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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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2032.4
241.2
241.2
196.6
196.6
195.6
                                                                                                            174
162.4
162.4
162.4
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    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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seq length: 200000000
                                                                                                                                                                100.0
99.8
99.3
99.1
11.8
11.8
9.6
9.5
9.5
7.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-806-197-1
2052
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gb in:
gb in:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                   GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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                                E40089
AR076817
E15125
AR076816
E15124
AR146852
E55065
E05188674
BD188674
BD188674
BD188674
BD188674
AR146856
AR146856
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E40093
E40091
E40090
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11124.566 Million cell updates/sec
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E40087 Plant promo
E40093 Plant promo
E40091 Plant promo
E40090 Plant promo
E40090 Plant promo
E40090 Plant promo
AR076817 Sequence
E15125 Promoter: 7
AR076816 Sequence
E15124 Promoter: 7
AR146852 Sequence
E55065 Plant promo
T18706 Daucus caro
E0188672 Promotor
E0188674 Promotor
E016255 Carrot gCHS
AR146856 Sequence
AR146875 Sequence
E55069 Plant promo
E55069 Plant promo
E55070 Plant promo
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90.6	90.6	90.6	90.8	91	91	91	91.6	91.8	92.4	92.6	92.6	93	93.8	95.2	95.8	96.4	96.4	96.6	97	99.2	99.4	100.4	101.8		106.6
4.4	4.4	4.4	4.4	4.4	4.4	4.4		4.5	5	4.5		4.5	4.6	4.6	4.7	4.7	4.7	4.7	4.7				5.0	5.0	5.2
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CR847802	AC104073	AC104069	PFMAL3PS	CR392006	AC126283	YSCMTCG13	AX599046	AX598900	CR356223	PFMAL4P3	CR388025	AX344555	AC091214	PFA929352	AL928596	DMU37541	DMU11584	PFMAL1P3	AE001398	AC105425	AX599046	CR382399	AE014832	AC093899	AE014839
CR847802 Danio rer	AC104073 Homo sapi	AC104069 Homo sapi	AL034556 Plasmodiu	CR392006 Danio rer	AC126283 Homo sapi	L36897 Saccharomyc	AXS99046 Sequence	AX598900 Seguence	CR356223 Danio rer	AL035476 Plasmodiu	CR388025 Danio rer	AX344555 Seguence	AC091214 Homo sapi	AL929352 Plasmodiu	AL928596 Human DNA	U37541 Drosophila	U11584 Drosophila	AL031746 Plasmodiu	AE001398 Plasmodiu	AC105425 Homo sapi	AX599046 Sequence	CR382399 Plasmodiu	AE014832 Plasmodiu		AE014839 Plasmodiu

ALIGNMENTS

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RESULT 1
E40087
LOCUS
DEFINITION
ACCESSION
VERSION
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ORGANISM
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                                                                           Query Match
Best Local Similarity
Matches 2052; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
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                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                           OS Daucus carota L.
PN JP 2000166577-A/1
PD JP 2000166577-A/1
PD 20-JUN-2000
PF 01-OCT-1999 JP 1999281475
PR SATOMI NISHIKAWA, KENJI OEDA
PC C12N15/09,A01H5/00,C12N1/21,C1
CC12N15/00, (C12N5/00,C12R1:91)
PC C12N5/00, (C12N5/00,C12R1:91)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 2052)
Nishikawa,S. and Oeda,K.
Plant promoter and terminator
Patent: JP 2000165577-A 1 20-JUN-2000;
SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E40087.1 GI:18627203
JP 2000166577-A/1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified
                             CATGTGTGCCCTACAGCACATAGGGCCTGTTTGGTTGAGAGAAGCAGAAGCTGCTTCTGA 60
CATGTGTGCCCTACAGCACATAGGGCCCTGTTTGGTTGAGAGAAGCAGAAGCTGCTTCTGA
                                                                           100.0%; ilarity 100.0%; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                  SATOMI NISHIKAWA, KENJI OEDA
C12N15/09, A01H5/00, C12N1/21, C12N5/10//(C12N5/10, C12R1:91), PC
                                                                                                                                                                          /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                             0,
                                                                                                                                                                                                                                                                                 Location/Qualifiers (1). (2052).
                                                                             Score 2052; DB 6;
Pred. No. 4.4e-310;
; Mismatches 0;
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                                                                                                                   Length 2052;
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1021 TGATCATCCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAA 1080	•						2 2 2	41	81		61	0 10		81 TCTCATTTCTACTCCACTTCTTTGCTATAAGCAAGAAATCACTTCTTTTAAGCTAACCCA		61 CTTCTTCTTCTTTGACCTGTTTGTATAAAGAAGTAGAAATATTTTTAAAAAGCTGCGAA 120
							<u> </u>									
RESULT 2 E40093 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	Db 2	Db Qy	Db 04	g gy	B 8	B &	Db Oy	dg dg	D Qy	B &	Db Qy	Qy Db	D 29	Qy	B &	Db
E40093 Plant promoter and terminator. E40093 E40093.1 GI:18627209 JP 2000166577-A/7. unidentified	2041 ATTCTAAATATC 2052 2041 ATTCTAAATATC 2052	1981 CACATCAATCTTACACCACAAACCTTGAGCTTAATTTTTCTACTTACT	1921 AACACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACTATCAT 1980 	1861 GATTGGAATCCTTTTCTAAACTTTTAAAATAAAAAAATGCATTATTGTAATATTTATC 1920 	1801 GCATTCTAGAATACATCTTTTCAAATTTCAACAAAACACAGCTTTAACTTTTCTTTC	1741 GTTTGAACAATGTATGTCCGGTGTACATCTATGACCTTTCAACTCAAACTAGTGAATAAT 1800 	1681 AATTTAAAATAATTATTGAGCATGGGAAGTTCACGGGCATCATTGAGCAGCACTAGACT 1740 	1621 TGTATTCAATAGTTTTAATATAAAAGTAAATTTAAATTAAATTGTTTATTTTTGTTTCAGA 1680 	1561 TTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATG 1620	1501 CTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATGAATAAATCAG 1560	1441 TAAGATTATAAATCTATGTTATAATGATAATAATATTATAAAAATAATACTATATTAAAT 1500 	1381 TAAATGGGACAGAGGGAGTAATACCTTTATGATATATAAATTTTTGTTATTTTGATTTCA 1440 	1321 AGAAAGTITTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGAAAGTGTATAGAAT 1380 	1261 AAAAGTAGTTGAAAGTAGTGGGTGGGTGGGATTTTTATATTAT		1141 ATACATATGGATTGGACACGAGACTVAGGAAAAATTTATAAAGTAATTGTAGAGTAAAAAA 1200

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REFERENCE
AUTHORS
TITLE
JOURNAL
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Best Local Similarity
Matches 2050; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unclassified.

1 (bases 1 to 2052)
Nishikawa,S. and Oeda,K.
Plant promoter and terminator
Patent: JP 2000166577-A 7 20-JUN-
SUMITOMO CHEM CO LTD
OS DAUCUS CATOTA
PP 2000166577-A/7
PD 20-JUN-2000
PP 01-OCT-1999 JP 1999281475
PR SATOMI NISHIKAWA,KENJI OEDA
PC C12N15/09,A01H5/00,C12N1/21,
C12N15/00, (C12N5/00,C12N1/21,
PC C12N15/00, (C12N5/00,C12N1/21,
C12N15/00, (C12N5/00,C12N1/21,
C12N15/00, (C12N5/00,C12N1/21,
C12N15/00, (C12N5/00,C12N1/21,
PC C12N15/00, (C12N1/20,C12N1/21,
PC C12N15/00, (C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C12N1/20,C
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                                                                                                                                                                                                                                                                                                    CCGTCTTCCAAGATAATATATTTTAATTTTGTAGCCTCCCTTTTAACCAAATTCGCATGC
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                                  AAAATTCCCGTTTAACCAGTTTGTTAATATATATATGTTTACACTTACAAGAGGGATATTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATGTGTGCCCTACAGCACATAGGGCCTGTTTGGTTGAGAGAAGCAGAAGCTGCTTCTGA
                 AAAATTCCCGTTTAACCAGTTTGTTAATATATATGTTTACACTTACAAGAGGATATTCGT
                                                                                                  TGGCCGAATGCTTCTCAAAATGTTTTTTATATGTAAAATAATGCCCATCCAAGGATAAGT
                                                                                                                                                  ATGCTCAGCCATCAAAATTGACAAAACCCGACACACACTCTATCCACGTACTATACTTT
                                                                                                                                                                   ATGCTCAGCCATCAAAATTGACAAAACCCGACACACACTCTATCCACGTACTATACTTT
                                                                                                                                                                                                                   AGGACGACTTAGGTGAATACACATTGTACTGTGAGTCTTTAAACAAAGAACAAGTGGTTC
                                                                                                                                                                                                                                   AGGACGACTTAGGTGAATACACATTGTACTGTGAGTCTTTAAACAAAGAACAAGTGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                  AACGGCCTCAATAAAAGATCATTCATAAATGTATCTTTCAATTTTAGGATAACAATACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SATOMI NISHIKAWA, KENJI OEDA
C12N15/09,A01H5/00,C12N1/21,C12N5/10//(C12N5/10,C12R1:91),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C12N5/00, (C12N5/00, C12R1:91)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. 1.4e
0; Mismatches
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les 2;
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		SOURCE unidentified ORGANISM unidentified unclassified. REFERENCE 1 (hasa 1 to 2050)
	r. DNA linear PAT 31-JAN-2002	ITION Plant promoter and termi SION E40091 ON E40091 GI:18627207 RDS JP 2000166577-1/6
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Nishikawa,S. and Oeda,K.
Plant promoter and terminator
Patent: JP 2000166577-A 4 20-JUN-2000;
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Best Local Similarity
Matches 2048; Conserv
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PD 20-JUN-2000

PF 01-OCT-1999 JP 1999281475

PR SATOMI NISHIKAWA, KENJI OEDA

PC C12N15/09, A01H5/00, C12N1/21, C1

C12N15/00, (C12N5/00, C12R1:91)

PC C12N5/00, (C12N5/00, C12R1:91)

CC C12N5/00, (C12N5/00, C12R1:91)
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   TGGTCACTGATAAATAGATAATTGTTAGTATAATATAGTAGGATCTACAATGACATTAAA
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C12N15/09, A01H5/00, C12N1/21, C12N5/10//(C12N5/10, C12R1:91), PC
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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AUTHORS
TITLE
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Plant promoter and terminator
Patent: JP 2000166577-A 3 20-JU
SUMITOMO CHEM CO LTD
OS Daucus Carota L.
PN JP 2000166577-A/3
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JP 2000166577-A/3.
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PN JP 2000166577-A/3

PD 20-JUN-2000

PF 01-OCT-1999 JP 1999281475

PR PI SATOMI NISHIKAWA, KENJI OEDA

PC C12N15/09, A01H5/00, C12N1/21, C12N5/10// (C12N5/10, C12R1:91),

CC C12N15/00,

PC C12N5/00, (C12N5/00, C12R1:91)

PC C12N5/00, C12N5/00, C12R1:91)
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Best Local Similarity 72.8%;
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Torikal, S. and Oeda, K.
Plant promoter and utilization thereof
Patent: US 5959176-A 2 28-SEP-1999;
Location Qualifiers
1. 2042

/organism="unknown"
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patent US 5959176.
Score 241.2; DB 6
Pred. No. 3.7e-28;
0; Mismatches 128
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Torikai, T. and Oita, K.

RES TORIKAI, T. and Oita, K.

VEGETABLE PROMOTER AND ITS USE

PALENT: JP 198052273-A 2 24-FEB-1998;

SUMITOMO CHEM CO LTD

OS Daucus carota L. (carrot)

PN JP 1998052273-A/2

PN JP 199805273-A/2

PN JP 1998052273-A/2

PN JP 1998052273-A/2

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PN JP 199805273-A/2

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JP 1998052273-A/2.
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                                                                                                                /organism='Daucus oter 1<..<2042.
                                    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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AR076816
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Best Local Similarity 72.8
Matches 367; Conservative
1864 TGGAATCCTTTTCTAAACTTTTTAAAATAAAAAAAATGCATTATTGTAATATTTATCAAC
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Unknown.
Unclassified.
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                                                                                                                                                                                                                                                                                           1 (bases 1 to 247)
Torikai,S. and Oeda,K.
Plant promoter and utilization thereof
Patent: US 5959176-A 1 28-SEP-1999,
Location/Qualifiers
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Sequence 1 1
AR076816
AR076816.1
                                                                                                                                                                     Similarity
                                                       CTCAGCAATAACATTCTAAATATC
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                                                                                                                                          9.6%;
nilarity 89.6%;
Conservative (
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/mol_type="unassigned
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                                                                                                                                    Score 196.6; DB 6;
Pred. No. 4.9e-21;
0; Mismatches 24;
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Pred. No. 3.7e-28;
0; Mismatches 128;
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FEATURES

247; 2

Gaps

PAT

30-AUG-2000

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1840 1848 1780 1789

COMMENT

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1 (bases 1 to 247)

1 (bases 1 to 247)

TOTIAE VEGETABLE PROMOTER AND ITS USE
VEGETABLE PROMOTER AND ITS USE
JOURNAL SUMITOMO CHEM CO LTD
OS DAUGUS CARCTA L. (CARTOL)
PN JP 1998052273-A/1
PD 24-FEB-1998
PF 12-AUG-1996 JP 1996212680
PI TORIKAI TOSHIMI, OITA KENJI
PC C12N15/09,A01H5/00,C07H21/04,C07K14/415,C12N1/21,C12N5/10; CC
Strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key
FT Source 1. 2^-
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Best Local Similarity
Matches 223; Conserv
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                                                                                                                                                                       TGGAATCCTTTTCTAAACTTTTTAAAATAAAAAAATGCATTATTGTAATATTTTATCAAC
                                                   ACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACCTATCATCAC 1983
                                                                                            TAGAAT COTTTCCTAAACTTTTAAAATT -- AAAAAATACATTACTATAATATTTATCAAC
                                                                                                                                                      TTCTAGAATATATCTTTTGAAATTTCAACAAACACAGCACTAACTTTTCTTTTAACAGAT
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       ATCAATCTTACACCACAAACCTTGAGCTTAATTTTTCTACTTATTCTCAGCAATAACATT 2043
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                                                                                                                                                                                                           9.6%;
nilarity 89.6%;
Conservative
                                                                                                                                                                                                                                                                               /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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                                                                                                                                                                                                            Score 196.6; DB 6;
Pred. No. 4.9e-21;
0; Mismatches 24;
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AR146852
LOCUS
DEFINITION
ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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E55065
LOCUS
DEFINITION
ACCESSION
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Best Local :
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           Plant promoter
Patent: JP 2000083679-A 2 28-MAR-2000;
SUMITOMO CHEM CO LTD
OS Daucus carota L.
PN JP 2000083679-A/2
PD 28-MAR-2000
PF 12-JUL-1999 JP 1999197240
PR
PI IKUHARU ISHIGE,SATOMI NISHIKAWA,KENG
PC C12N15/09,A01H5/00,C12N1/21,C12N5/10
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Patent:
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1 (bases 1 to 246)
1 shige, I., Nishikawa, S. and Oeda, K.
                                                                                                                                                                                        unidentified
                                                                                                                                                                                                             Plant promoter.
E55065
E55065.1 GI:18625251
JP 2000083679-A/2.
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Ishige, F., Nishikawa, S. and Oeda, K.
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Similarity 89.5%;
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IKUHARU ISHIGE, SATOMI NISHIKAWA, KENJI OEDA
C12N15/09, A01H5/00, C12N1/21, C12N5/10//(C12N15/09, C12R1:91),
(C12N5/10, C12R1:91), C12N15/00, C12N5/00, (C12N15/00, C12R1:91),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
/mol_type="unassigned DNA"
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patent US 6218598.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 195.6; DB Pred. No. 7e-21;
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RESULT 12
DCA18706/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239
                                                                                                                                                                                                                                             Submitted (27-JAN-1999) A. Sturm, Maulbeerstr. 66, CH-4058 Basel, Strelated sequence X67163.
                                                                                                                                                                                                                                                                                                                                    Molecular characterisation and functional analysis of sucrose-cleaving enzymes in carrot (Daucus carota L.) J. Exp. Bot. 47, 1187-1192 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Apiales; Apiaceae; Apioideae; Scandiceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta-fructofuranosidase; Inv*Dc5 gene; invertase; isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Daucus carota (carrot)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y18706.1 GI:4454114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Daucus carota Inv*Dc5 gene.
Y18706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (C12N5/00,C12R1:91)
CC
FH Key
FT Source
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ilarity 89.5%;
Conservative
               /gene="Inv*Dc5"
}oin(2767. .3160,3724. .3732,4656. .5515,5605. .5766,
$869. .6104,6190. .6277,6384. .6587)
                                                                                                                                                                                                                1. .8005
                                                                                                                                                       /organism="Daucus carota"
/mol_type="genomic DNA"
/cultivar="Nantaise"
                                                                                                   gene="Inv*Dc5"
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                                                                                                                                                                                                                               ocation/Qualifiers
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unidentified"
/mol_type="genomic DNA"
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                                                                                     .2666
                                                                                                                                        xref="taxon:4039"
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Pred. No. 7e-21;
0; Mismatches :
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SWITZERLAND
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                                                  1285
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CACTATGGGGGTGTTTGTTTCCCGGAAGTAGGAGCTGCTTCCGTCTTCTGCTTTGA 1226
                                                                     CACATAGGGCCTGTTTGGTTGAGAGAAGCAGAAGCTGCTTCTGACTTCTTCTTCTTTTGA
                                                                                                                    8.5%; Score 174; DB 8; Length 8005; llarity 81.7%; Pred. No. 8.2e-18; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                         6384. .6587
                                                                                                                                                                                                                                                                                                                                                                                                    6190.
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                                                                                                                                                                                                              'gene="Inv*Dc5"
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stlaaclumgtmylfpenggneryekstyvpeetyvevaprgvaegvsmksfrrpalnae
ppamepmsnylswqrsfeprognmeryekstyvpeetyvevaprgvaegvsmksfrrpalnae
ppamepmsnylswqrsfeprognmeryekstyvpengleyqyrpdgrifgynkti
wghavsblihwkih.pvamytdhwydvngybygsatiepytgyrybgrybistysvqv
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QNLAYPADPSDPLLIEWKYPGNPVLVPPPGIDFKDFRDFYPVSKFGENGLDTSFDGVG
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WKTVERNVEINTGAVLPLEIGSGSQLDITAEFEVDKSSLERVQETNRVYDCKNNGGSS
GRGALGPFGLLILADKDLSEGTPVFFIAKGSGGNLRTFFCADHSRSSKADDVDKEIY
GRGALGPFGLLILADKDLSEGTPVFFIAKGSGGNLRTFFCADHSRSSKADDVDKEIY
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ARIIASLNIWQMVTAQRQTHFADLVI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="Inv*Dc5"
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gene="Inv*Dc5"
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/gene="Inv*Dc5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="beta-fructofuranosidase, isoform II"
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/db_xref="GOA:042715"
/db_xref="GOA:042722"
/db_xref="UniProt/TremBL:042722"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    number=1
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/EC_number="3.2.1.26"
/note="soluble acid invertase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

FEATURES COMMENT

5'UTR gene

<u>.</u>

Gaps

76

REFERENCE AUTHORS TITLE

VERSION KEYWORDS

FOCUS

DEFINITION

CCESSION

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FEATURES

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RESULT 14
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Best Local Similarity
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             BD188674
Promotor
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Promotor and use thereof.
                                                                                                                                                                                                                                             AGGGCCTGTTTGTTTTATGGAATCAGAAGCTGCTTCTGACTTCTGCTTTTTTT-ACCCGT
                                                                                                                                                                                                                                                               AGGGCCTGTTTGGTTGAGAGAAGCAGAAGCTGCTTCTGACTTCTTCTTTTGACCTGT
                                                                                                      TTGCTATAAGCAAGAAATCACTTCTTTTAAGCTAACCCAAACGGCCTCAATAAAAGATCA
                                                                                                                                         TICTGCTTCTTTTCCAAACACTTTATCAACTTACCTACTTCTCACTTCTGCTTCACTTCT
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31-MAY-2001 JP 2001164069
8ATOMI NISHIKAWA, KENJI OEDA
C12N15/09,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/
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llarity 82.5%;
Conservative
              and use thereof.
                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. 6.4e-16;
0; Mismatches 41;
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Lified

Liassified.

1 (bases 1 to 2865)

Nishikawa, S. and Oeda, K.

Promotor and use thereof

JOURNAL

SUMITOMO CHEMICAL CO LTD

OS Daucus Carota L. (carrot)

PN JP 200300252-A/3

PD 07-JAN-2003

PF 31-MAY-2001 JP 20011c

PI SATOMI NISHIKAWA "

PC C12N15/09,A01"

PC O0,C12N5/c"

CC Promot
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KEYWORDS
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Direct Submission

Submitted (14-MAY-1993) Yoshihiro Ozeki, College of Arts and Sciences, The University of Tokyo, Department of Biology; Kor Meguro-ku, Tokyo 153, Japan (Tel:03-3467-1171(ex.253),
                                                                                     1 (bases 1 to 4886)
Ozeki,Y., Davies,E. and Takeda,J.
Structure and expression of chalcone synthase suspension cultured cells regulated by 2,4-D plant Cell Physiol. 34, 1029-1037 (1993)
                                                                                                                                                                                                   Carrot gCHS2 gene for chalcone synthase.
116255
116255.
116255.1 GI:441168
chalcone synthase.
Daucus carota (carrot)
Daucus carota
                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Apiales; Apiaceae; Apioideae; Scandiceae;
                                                               Ozeki,Y.
                                                                                                                                                                                                                                                                                   DARGCHS2
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31-MAY-2001 JP 2001164069
SATOMI NISHIKAWA, KENJI OEDA
C12N15/09, A01H5/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. 6.4e-16;
0; Mismatches 41;
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Yoshihiro Ozeki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Codon start=1
/ Codon start=1
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QGCRAGGTVLRLAKDLAENNKOARVLLVYCSSITVITFRGPNDTHLDSLVGQALFEDG
RANIFKSIVEAFKPLGISDMNSIFWIAHPGGPAILDQVETELSLKPEKLKSTRQVLRDY
GNMSSACVLFILDEMRKASAKDGHRTTGEGILDWGVLFGFGPGLTVETVVLHSVPT"
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/note="G-box"

2303. .2308

/note="TACPYAT motif"

2327. .231

2358. .4519

/note="CHS2 mRNA and intron"

2358. .2607
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4501. .4506
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3395. .4519
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/db_xref="taxon:4039"
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Search completed: March 15, 2005, 13:22:00 Job time: 8943.89 secs

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           0 0 0 0
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                                                                                   Aav15143 New promo
Aaz49611 Carrot CR
Adp07499 Carrot DN
Adc56759 Carrot DN
Adc56761 Carrot DN
                            Aaz49616
Aaz49615
Abz10246
Abz10100
Abz101046
Abz10246
                                                                                                                          Aav15144
Aav15143
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          Abz10100 Haematopo
Continuation (7 of
                                                                                                                                              Aaa37963
                                                                                                                                                        Aaa37962
                                                                                                                                                                          Aaa37961
                            6 Oligonucl
6 Oligonucl
6 Haematopo
7 Haematopo
7 Haematopo
7 Carrot te
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Carrot p
Plasmid
Plasmid
Plasmid
                                                                                                                                  New promo
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Ads89551 Oligonucl	ADS89551	13	5286	3.3	67.4	45		
Abl34011 Human imm	ABL34011	σ	6050	3.3	67.6	44		
Abq66994 Human ang	ABQ66994	Φ	5984	3.3	67.6	43		
Abd32992 Human can	ABD32992	13	99764	3.3	67.8	42	a	
Abk28233 DNA trans	ABK28233	δ	15732	3.3	67.8	41	a	
	AAS45388	4.	15732	J. J.	67.8	40	a	
	ABL32218	6	11422	υ . υ	68	39		
Abk39936 Human che	ABK39936	σ	11422	<u>د</u> .	68	38		
6 Continuation (7 of	ABD32968_	13	110000	3.3	68.2	37		
Abl34155 Human imm	ABL34155	σ	15548	ω 	68.2	36	a	
Abl70624 Chemicall	ABL70624	D	6045	3.4	69.2	ω Ç		
Abk31541 Signal tr	ABK31541	σ	6045	3.4	69.2	ω 4		
Abl70376 Chemicall	ABL70376	6	16258	3.4	69.4	ω ω	ი	
Abk40038 Human che	ABK40038	0	16258	3.4	69.4	32	a	
Adb54190 Pretreate	ADB54190	10	11222	3.4	69.6	31	ი	
Acf62794 Colon can	ACF62794	œ	8222	3.4	69.6	30	Ω	
Aas61235 Human gen	AAS61235	σ	6352	3.4	69.8	29		
Abl70563 Chemicall	ABL70563	σ	6352	3.4	69.8	28		
Abk31340 Signal tr	ABK31340	σ	6352	3.4	69.8	27		
Ads89552 Oligonucl	ADS89552	13	5286		70.8	26	ი	
Ads89278 Oligonucl	ADS89278	13	5286	<u>3</u> .5	70.8	25	ი	
Abl32517 Human imm	ABL32517	σ	5930		71	24	ი	
Adb54318 Pretreate	ADB54318	10	11222		71.2	23	ი	
Acf62816 Colon can	ACF62816	œ	8222	3.5	71.2	22	O	
Abk28332 DNA trans	ABK28332	σ	11745	3.7	75	21	a	

ALIGNMENTS

RESULT 1
AAA37959
ID AAA37959
ID AAA37959
ID AAA37959
ID AAA37959
ID AAA3
AC AAA3
AC AAA3
AC Carr
XX Carr
XX Carr
XX Carr
XX Dauc
XX Dauc
XX Dauc
XX Dauc
XX Dauc
XX Dauc
XX PD 13-A
XX DAUC
PF 10-A
XX PF 28-S
XX PF 28-S
XX PF 10-A
XX Carr
XX Carr
XX Carr
XX Dauc
XX Thish
XX PF New
PT Plar
XX Clai
XX Thish
CC Off Cor the
CC Thish
CC Thi Nishikawa S, Carrot; promoter; terminator; transgenic plant; breeding; fertility; ds. AAA37959; 02-OCT-1998; 28-SEP-1999; 13-APR-2000 WO200020613-A1 Daucus carota. Carrot promoter sequence 18-AUG-2000 AAA37959 standard; (SUMO) SUMITOMO CHEM CO LTD. (first entry) Oeda K; 98JP-00281124. 99WO-JP005303. DNA; 2052 #1. ΒP

This sequence represents a carrot promoter. The invention relates to plant promoters and terminators from Daucus carota L. which are capable of expressing a gene of interest in plants. The invention also includes a chimeric gene characterized in that it comprises the promoter and a desired gene linked to each other in the form capable of functioning. A method of producing a transformant comprises introducing the promoter, the chimeric gene or a vector comprising the promoter and a desired gene or terminator sequence into a host cell. The plant promoters and terminators are useful in plant breeding, for e.g. fertilities of plants may be controlled by expressing, in the host cells, a sense or antisense

New Plant promoters and terminators from Daucus carota $L_{\cdot,\cdot}$ useful plant breeding, for e.g. controlling fertilities of plants.

WPI; 2000-303791/26.

Claim 1; Page 69-70; 81pp; English.

odq 1

**	CC XX SQ Que Bes
CINES 2032; CORSEIVALIVE 1 1 CATGTGTGCCCTACAGCACA	gene of a m Sequence 20 Y Match
	Qy Db
1021 1681621CCAPTINAMICCITTITINAMICMATTCALTGATIANT TITLE TITLE TO THE ANGARGACANTATITITICAL CONTROL TO THE ANGARGACANT TITLE TITLE TO THE ANGARGACANT TITLE TO THE ANGARGAN ANGARGACANT TITLE TO THE ANGARGAN ANGARGAN ANGARGAN TITLE TO THE ANGARGAN ANGARGA	

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RESULT 2
AAA37961
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a carrot promoter. The invention relates to plant promoters and terminators from Daucus carota L. which are capable of expressing a gene of interest in plants. The invention also includes a chimeric gene characterized in that it comprises the promoter and a desired gene linked to each other in the form capable of functioning. A method of producing a transformant comprises introducing the promoter, the chimeric gene or a vector comprising the promoter and a desired gene or terminator sequence into a host cell. The plant promoters and terminators are useful in plant breeding, for e.g. fertilities of plants may be controlled by expressing, in the host cells, a sense or antisense gene of a male sterility related gene such as S-locus-specific RNase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 78-79; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                        CATGTGTGCCCTACAGCACATAGGGCCTGTTTTGGTTGAGAGAAGCAGAAGCTGCTTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2052 BP; 736 A; 318 C; 317 G; 681 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                      CTTCTTCTTTTGACCTGTTTGTATAAAGAAGTAGAAATATTTTTAAAAAGCTGCGAA
                    AACGGCCTCAATAAAAGATCATTCATAAATGTATCTTTCAATTTTTAGGATAACAATACGT
                                                                                               TCTCATTTCTACTCCACTTCTTTGCTATAAGCAAGAAATCACTTCTTTTAAGCTAACCCA
                                                                                                                                                                                         TACTAACTTCTCTCTCACAACTTCCGCTTCTTTTCCAAACACTTTATTAACTTTTTACT
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                                                                       ACTCCACTTCTTTGCTATAAGCAAGAAATCACTTCTTTTAAGCTAACCCA
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Query Match
Best Local Sim
Matches 2050;
                                                                                  This sequence represents a plasmid sequence used in a method for introducing a mutation into a carrot promoter. The invention relates to plant promoters and terminators from Daucus carota L. which are capable of expressing a gene of interest in plants. The invention also includes a desired gene characterized in that it comprises the promoter and a method of producing a transformant comprises introducing the promoter, the chimeric gene or a vector comprising the promoter and a desired gene to the reminator sequence into a host cell. The plant promoters and terminators are useful in plant breeding, for e.g. fertilities of plants may be controlled by expressing, in the host cells, a sense or antisense gene of a male sterility related gene such as S-locus-specific RNase gene
                                                                  Sequence 2056 BP;
                                                                                                                                                                                                                                                                                                                                    Example 8; Page 74-76; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                   New Plant promoters and terminators from Daucus carota L., plant breeding, for e.g. controlling fertilities of plants
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CC gene Carrot; promoter; Plasmid #1 DNA sequence used 02-OCT-1998; 28-SEP-1999; 13-APR-2000. WO200020613-A1 Daucus carota. 98JP-00281124 99WO-JP005303 terminator; transgenic plant; breeding; fertility; ds. in mutation of promoter sequence

WPI; 2000-303791/26 Nishikawa (SUMO) SUMITOMO CHEM တ 0eda ζ, ဗ CLID

New Plant promoters and terminators from Daucus carota L., useful plant breeding, for e.g. controlling fertilities of plants. in

8; Page 71-73; 81pp; English.

This sequence represents a plasmid sequence used in a method for introducing a mutation into a carrot promoter. The invention relates to plant promoters and terminators from Daucus carota L. which are capable of expressing a gene of interest in plants. The invention also includes a chimeric gene characterized in that it comprises the promoter and a desired gene linked to each other in the form capable of functioning. A method of producing a transformant comprises introducing the promoter, the chimeric gene or a vector comprising the promoter and a desired gene or terminator sequence into a host cell. The plant promoters and terminators are useful in plant breeding, for e.g. fertilities of plants may be controlled by expressing, in the host cells, a sense or antisense gene of a male sterility related gene such as S-locus-specific RNase gene

Sequence 2048 BP; 735 A; 317 C; 316 G; 680 T; 0 U; 0 Other;

Query Match Best Local Similarity 99.0**%;** 99.7**%**; Score 2030.8; Pred. No. 0; DВ ω --Length 2048;

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                                    GAACAGGGTTATTTTTAACGTGTCAACAAATTCTAATAATTTTACCTGGCCGGTGAACA
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  WPI; 1998-122310/12
                                             Torikai S,
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                                                                                                                                                                                                                                                                                                  Daucus carota,
                                                                                                                                                                                                                                                                                                                                                               Promoter; root; oplant cell; soil
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pathogen; improve; nutritive value; edible root plant;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a novel promoter, and is isolated from the roots of carrots, cultivar Kuroda Gosun. The promoter can be used to direct root-specific expression in plant cells. Since the promoter enables expression of a desired protein in the roots of a plant, it is useful in combat against pathogenic soil fungi and pests which are difficult to kill by chemicals. It can also be used to improve the nutritive value of edible root plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2042 BP; 719 A; 356 C; 323 G; 644 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New carrot root gene, promoter and terminator - useful in engineering for directing root-specific gene expression.
    2019
                                                          1959
                                                                                    1969
                                                                                                              1899
                                                                                                                                                                  1841
                                                                                                                                        1909
                                                                                                                                                                                            1849
                                                                                                                                                                                                                                                                                                                                1661
                                                                                                                                                                                                                                                                                                                                                                                                                                       1543
                                                                                                                                                                                                                                                                                                                                                                                                                                            1554 AAATCAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCG----TTCGGTCAAATG
               CTCAGCAATAACATTCTAAATATC
                                                                                                 ATAATATTTATCAACACCTCAACATTCATGTTAGCGTACTATAAATAGGTGCTCTTGGTG
TTTAGCAAAAACATTCTAAAGGTC
                                           ĊŦĊŦĀĊŦĀŦĊĀŦĊĀĊĀŦĊĀĀŦĊŦŦĊĊĀĠĊĀĊĀĀĀĊĊŦŦĠĀĠĊŦŦĀĀŦĊŦŦŦĊŦĀĊŖŦĀĀŦ
                                                              CTCTACTATCATCACATCAATCTTACACCACAAAACCTTGAGCTTAATTTTTCTACTACTATT
                                                                                                                  GTAATATTTATCAACACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTG 1968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 72.6
66; Conservative
                                                                                                                                                     TTTCTTTAACAGATTAGAATCGTTTCGTAAACTTTTAAAATT--AAAAAATACATTACT
                                                                                                                                                                        TÁGCCÁGTGAÁTĠCTŤŤĊŤÁĠÁÁŤÁTÁŤCŤŤŤTGAÁÁŤŤŤCAÁCÁAÁČÁČÁCÁĠĊACŤÁÁĊŤ
                                                                                                                                                                                                                                                               CACGTTGTATTGTTTAAACAACGTTTGTCCGGTGTATATTTATGACCTTTCAACTCAAGC
                                                                                                                                                                                                                           AGCACTAGACTGTTTGAACAATGTATGTCCGGTGTACATCTATGACCTTTCAACTCAAAC
                                                                                                                                                                                                                                                                                                                   ATAAGTTAATTCTTCAATCAATTAACTTTAAATTTTGGACATTATTGAGCAACTTTATGCC
                                                                                                                                                                                                                                                                                                                                            TTTGTTTCAGAAATTTAAAATTAATTGAGCATGGGAAGTTCACGGGCATCATTGAGC
                                                                                                                                                                                                                                                                                                                                                                      CCAAGTTCACGTGTÄTTCTAAÅATGTTÄÄTÄCTÄÄCATGÄGTATTTTCTT--TTCAAGGT
                                                                                                                                                                                                                                                                                                                                                                                               AAATTATTTATCTGAATGATAACATCTTTGTAAACAAAACTGCGCCAAATAGGACCATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 15-16; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; 72.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 239.6; DB 2
Pred. No. 8.7e-35;
0; Mismatches 129
2042
                        2052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genetic
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AAV15143
ID AAV15143;
XX AAV15143;
XC AAV15143;
XC AAV15143;
XX DT 02-JUL-1998 (first entry)
XX XX

XX

DE New promoter used for root-specific expression in plants.
XX

Promoter; root; carrot; Kuroda Gosun; root-specific expression;
XX

RW Promoter; root; carrot; improve; nutritive value; edible root plant;
XX

XX

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Daucus carota.
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Best Local Similarity
Matches 223; Conserv
                                                                       Synthetic DNA; plant promoter; CR16.3 fragment; soybean glycinin; stearoyl-ACP-desaturase gene; male sterility-related gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the roots of carrots, cultivar Kuroda Gosun. The promoter can be used to direct root-specific expression in plant cells. Since the promoter enables expression of a desired protein in the roots of a plant, it is useful in combat against pathogenic soil fungi and pests which are difficult to kill by chemicals. It can also be used to improve the nutritive value of edible root plants
                                                Daucus carota.
                                                                                                                          Carrot CR16.3
                                                                                                                                                   07-APR-2000
                                                                                                                                                                                                    AAZ49611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 247 BP; 88 A; 50 C; 21 G; 88 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a novel promoter, and is isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New carrot root gene, promoter and terminator - useful in genetic engineering for directing root-specific gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-122310/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-AUG-1996;
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                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGAATCCTTTTCTAAACTTTTTAAAATAAAAAAAATGCATTATTGTAATATTTATCAAC 1923
                                                                                                                                                                                                                                                                                                                                      ATCAATCTTACACCACAAACCTTGAGCTTAATTTTTCTACTTATTCTCAGCAATAACATT
                                                                                                                                                                                                                                                                                                                                                                                      ACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACTATCATCAC 1983
                                                                                                                                                                                                                                                                                                                                                                                                                       TAGAATCGTTTCCTAAACTTTTAAAATT--AAAAATACATTACTATAATATTTATCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTAGAATATATCTTTTGAAATTTCAACAAACACAGCACTAACTTTTCTTTTAACAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 14; 31pp; English.
                                                                                                                                                                                                                                                                  CTANAGGTC 247
                                                                                                                                                                                                                                                                                        CTAAATATC 2052
                                                                                                                                                                                                                                                                                                                  ATCAATCTTCCAGCACAAACCTTGAGCTTAATCTTTCTACTAATTTTTTAGCAAAAACATT
                                                                                                                                                                                                                                                                                                                                                                     ACCTCAACATTCATGTTAGCGTACTATAAATAGGTGCTCTTGGTGCTCTACTATCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oeda K;
                                                                                                                                                  (first entry)
                                                                                                                       fragment for synthesis of plant promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96JP-00212680
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                                                                                                                                                                                                    DNA;
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                                                                                                                                                                                                    246 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 196.6; DB 2
Pred. No. 5.8e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                 carrot;
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                                                                                                transgenic
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                                                                                                plant;
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RESULT 9
ADPO7499
ID ADPO7499
AC ADPO
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XX ADPO
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XX CAIT
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Best Local Similarity
Matches 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a CR16.3 fragment from carrot genomic DNA. It is used for synthesis of a plant promoter which comprises nucleotides 112-246, 54-246, or 1-246 of this sequence and a synthetic DNA. The promoter is used for controlling the expression of a desired gene e.g. soybean glycinin, stearoyl-ACP-desaturase and S-locus type specific RNase gene (male sterility-related gene) in a host cell especially a microorganism or a plant cell. The transformed plant cells can be used to produce transgenic plants. The promoter is compact and therefore suitable for higher expression of a desired gene in a particular tissue compared to
                                                                                                                                                                             Carrot; gene; transcription
                                                                              JP2004135597-A
                                                                                                                                                                                                                                                                       Carrot DNA
                                                                                                                                                                                                                                                                                                                                                                            ADP07499;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP07499 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 246 BP; 88 A; 50 C; 21 G; 87 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                         29-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishige F,
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                                                                                                                                carota.
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                                                                                                                                                                                   expression inducing prom
rt point; RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 196 BP
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89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 195.6; DB : Pred. No. 8.9e-27
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13-MAY-2004

18-OCT-2002;

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RESULT 10
ADC56759
XX ADC56
XX ADC56
XX ADC56
XX ACATO
XX CATO
XX CATO
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Best Local Similarity
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                       WPI; 2003-472920/45
                                                                                                                                                          31-MAY-2001; 2001JP-00164069
                                                                                                                 31-MAY-2001; 2001JP-00164069
                                                                                                                                                                                                                                                                                                            Daucus carota subsp.
                                                                                                                                                                                                                                                                                                                                                                                                              Carrot DNA that encodes an expression inducer type promoter.
                                                                     (SUMO ) SUMITOMO CHEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC56759 standard; DNA; 2831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an expression inducing promoter comprising a first DNA linked to a second DNA at its 5' terminus, where the first DNA has a region which determines a transcription start point of RNA polymerase II and has minimum promoter function, and the second DNA has expression inducing promoter function in a plant cell. The expression inducing promoter is useful for expressing a foreign gene. This sequence represents carrot DNA used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 4; 61pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expression inducing promoter, useful for expressing foreign gene, comprising first DNA for detecting transcription start point and having minimum promoter function, linked to second DNA having expression
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RESULT 11
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                                                                                          Disclosure;
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                                                                                                                                                                                                                                    WPI; 2003-472920/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Daucus carota subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carrot; expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC56761 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter. Specifically, it refers to promoter sequences derived from plant DNA, preferably carrot, and functional mutants thereof that can be used as expression inducers. Furthermore, the present invention describes DNA, vectors, transformants and the process by which to prepare transformants. This polynucleotide sequence is the DNA encoding the carrot promoter of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTACTATAAGCAAGAAGTCAATTCTTTTAAATTAACCCAAACGGCCCCTAAGTAATTTGA
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                                                                                          SEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding an expression inducer type promoter (SeqID 3).
                                                                                                                                                   inducer type promoter derived from
C. of 2831 bases and its analogues h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
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Pred. No. 1.5e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant; vector; transformant;
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                                                                                                                                                 m DNA of Daucus having the same
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This invention relates to carrot DNA used as an expression inducer promoter. Specifically, it refers to promoter sequences derived fro plant DNA, preferably carrot, and functional mutants thereof that c

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RESULT 12
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XX AAZ496
XX Oligon
XX Synthe
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XX DAUCUB
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The present sequence is an oligonucleotide (- chain) used to prepare a CR16.1 DNA fragment comprising nucleotides 112-246 of the carrot CR16.3 fragment. The CR16.1 DNA fragment is ligated to a 10 bp synthetic DNA for construction of a plant promoter. The promoter is used for controlling the expression of a desired gene e.g. soybean glycinin, stearoyl-ACP-desaturase and S-locus type specific RNase gene (male sterility-related gene) in a host cell especially a microorganism or a plant cell. The promoter is compact and therefore suitable for higher expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic DNA; plant promoter; CR16.1 fragment; carrot; trasoybean glycinin; oligonucleotide; stearoyl-ACP-desaturase male sterility-related gene; ss.
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                                                                                                                                                   Disclosure; Page 14;
                                                                                                                                                                                              Novel promoter used to
                                                                                                                                                                                                                                                                                                                  15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                               13-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                            02-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Daucus carota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide-4 for synthesis of CR16.1 fragment
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                                                                                                                                                                                                                                                                                      SUMITOMO CHEM
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                                                                                                                                                                                                                                                       Nishikawa
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                                                                                                                                                                                gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                  98JP-00200372
                                                                                                                                                                                                                                                                                                                                               99EP-00113732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
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82.5%;
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                                                                                                                                                   24pp; English
                                                                                                                                                                                                                                                                                      CO LTD.
                                                                                                                                                                                              produce transgenic
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Pred. No. 1.5e
0; Mismatches
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                                                                                                                                                                                              plants with higher expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carrot; transgenic plant;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 125;
                                   The present sequence is an oligonucleotide (+ chain) used to prepare a CR16.1 DNA fragment comprising nucleotides 112-246 of the carrot CR16.3 fragment. The CR16.1 DNA fragment is ligated to a 10 bp synthetic DNA for construction of a plant promoter. The promoter is used for controlling the expression of a desired gene e.g. soybean glycinin, stearoyl-ACP-desaturase and S-locus type specific RNase gene (male sterility-related gene) in a host cell especially a new gene (male sterility-related transformed plant cells can be used to produce transgenic plants. The promoter is compact and therefore suitable for higher expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic DNA; plant promoter; CR16.1 fragment; carrot; trasoybean glycinin; oligonucleotide; stearoyl-ACP-desaturase male sterility-related gene; ss.
                                                                                                                                                                 Disclosure; Page 13; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                          02-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                   EP976832-A2
                                                                                                                                                                                                                                                                                                                                                                                                           Daucus carota.
Synthetic.
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                          desired
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                                                                                                                                                                                                                                                                                                         15-JUL-1998;
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                                                                                                                                                                                         l promoter used to desired gene.
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                          gene in a
                                                                                                                                                                                                                                                                                SUMITOMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA; 140
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                                                                                                                                                                                                                                                       Nishikawa
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                                                                                                                                                                                                                                                                                 CHEM CO
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                         particular tissue compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          particular tissue compared to other host tissues
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92.6%;
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                                                                                                                                                                                                      produce transgenic plants with higher expression
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Pred. No. 1.
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                          to other host tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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Query Match Best Local Similarity Matches 125; Conserv

5.8%; llarity 92.6%; Conservative

0

Score 119; DB 3; Pred. No. 1.1e-12; 0; Mismatches 10

Length

Indels

0,

Gaps

0

Sequence

140

ВP;

44

A; 34 C; 17 G;

45 T; 0 U; 0 Other;

CC be us	CC relate CC ampl:									DR WPI;			PA (EPIG-)											SUL		B 1	0 D	8	Db Qy
be used for detecting a predisposition to, differentiation between also subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a	polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primars for the amplification of haematopoietic cell proliferation disorder the sequences. The nucleotide sequences from the record disorder related DNA sequences.	nining the cytosine methylation erace and location between acute mining the cytosine methylation erace and location in the cytosine erace and location in the cytosine erace and location erace and loca	invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferation.	distinguishes between methylated and non-methylated CpG leotides within the target nucleic acid. ABZ09861 to ABZ11118	subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the unifier with the larget nucleic acid in a	THE PRESENT INVENTION describes a method for detecting and differentiating between haematopoletic cell proliferative disorders	28; SI	nguishes between methylated and non-methylated CpG o	ting and differentiating between hematopoietic cell proliferative		Lipscher E, Ma I, Ziebarth H;	K, Braun A, Distler J, Guetig D, Howe A, Mueli Piepenbrock C. Adorian B. Graha Howe A, Mueli	3-) EPIGENOMICS AG.	26-MAR-2001; 2001US-0278333P.	26-MAR-2002; 2002WO-EP003401.	03-OCT-2002.	WO200277272-A2.	Homo sapiens.	cytosine methylation state; gene; ds.	n; haematopoietic cell proliferation disorder; cytostatic.	tic cell proliferation disorder related non-	ABALVA46; 16-JAN-2003 (first entry)	ABALUAN STANDARD; DNA; 8056 BP.	3			65 CATCACATCATCTTCCAGCACAAACCTTGAGCTTAATCTTTCTACTAATTTTTAGCAAA 124		1918 ATCAACACCTCAACATTGATGTTAGCGTACTATAAATAGGTGCTCTTTGGTGCTCTACTAT 1977
Db Qy	Db Qy	Db	Q g	B 8	Db	δ	Db !	OV D	. _Q	В	Q	Db	Ş	Db	δ	Db	ρ	DЬ	Qy	Db	Q (B 8	D	Qy	DЬ	νQ	Ma Be	SQ	×cc c
1442 AAGAITATAAATCTATGTTATAA 	1382 AAATGGGACAGAGGGAGTAATAC	2748 AAAATAAAAAAAATATTTAATTG	2692 TAAATTTATTATTTTTTTTTTTTTT 1322 GAAAGTTTTGAAATGTATAGAA		2632 AAAAATAAAAAAAAATGTTAAA!	1202 AAGAGAAAGAAAAGTGGGTAAA	2572 TTTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAA	2512 AATAAAAAAAATAAATTAAAT		2452 TTATTTTTATTTATATATTTT	1022 GATCATCCATTAAAACCTTGTT	2395 TATTTTTGAAAATTAAAAAAA	962 ТАРАССВАРАТСАТТТТАТАДО	2335 AATTTTATTTAATTTTTAAATI	902 AAACTGATCTAAAGCACATAG	5	848 GAGCTTGCTGCTGTGTGTTTA	2215 AAAAAAAAAATTTAATTTTA	788 CTATTAATTAAGTTACTAATA	2155 TAAAAAAAAAAAAATTATAA	728 TGATAAATAGATAATTATTTAAT	668 TTAGACGACAAGAGACTTAGG	2035 ATTTTTAAATATTTTTATT	608 CCGTTTAACCAGTTTGTTAAT	1975 ATTAATATTAATTTTATTT	- 14	Query Match 4.8%; Best Local Similarity 44.5%; Matches 624; Conservative 0	Sequence 8056 BP; 3711 A; 0 C	highly specific classificatio disorders allowing for improv

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; 371 G; 3974 T; 0 U; 0 Other;
                                                                                                        CTTTATGATATATAAATTTTGTTATTTTGATTTCAT 1441
                                                                                                                                                                                                                                                                                                                                                                                       TGAAAAAAAATTATAAATATAAATAATTAAAAAAA 2631
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Pred. No. 7.2e-09;
; Mismatches 761; Indels 18;
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                             TGATAATATAATTTTAAAAAATAATACTATATTAATTC 1501
                                                                           TATTTT--TTTATAAAATATTAAAAATTTGAAATTAT
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                                                                     Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent tidistinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
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 present invention describes a method for detecting and
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which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ0118 crepresent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative cdisorder haematopoietic cells; for differentiating between acute (1) ymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide collymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent,
disorders allowing for improved and informed treatment of patients
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Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;

Length

GACAATGTCTCTTTGAAAAAACAAATAGGTACTCCCTCCGTCCCTCTGAAATGTATACAT GATCTAAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAATTTATATTAAAC 966 TCCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAAAGAAG GAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACTGATCA CCCGTTTAACCAGTTTGTTAATATATATGTTTACACTTACAAGAGGATATTCGTAATACT AATGCTTCTCAAAATGTTTTTTATATGTAAAATAATGCCCATCCAAGGATAAGTAAAATT ATGGATTGGACACGGAGACTAAGAAAAATGTATAAAGTAATGTAGAGTAAAAAAGAAAGAG 1206 **AATTÄAAATTAATTÄCGTTATTATATTTTAATTAATAATAAATAAAATTTCGTTTTA** AGAGCTTGCTGTGTGTTTAGTTGTTGTGAGCTCATTTCTTTAAAAGTAATGTAAACT TAATTTTÄATÄTTTTÄAAÄÄATCGAÄÄTÄAÄCGAATCGTÄÄAÄTTÄÄAÄÄAAATTÄTTTT GCTATTAATTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAGCAGGTAAAAACA 846 CTGATAAATAGATAATTGTTAGTATAATATAGTAGGATCTACAATGACATTAAAATTAGA 786 **ATAÄTTAATTÄÄTTÄÄÄTTÄÄTÄTÄTÄTÄAATÄTAAAATATÄÄATÄČGTTÄÄAAAAATTT** TTTAGACGACAAGAGACTTAGGTCAAAAATGGACGCTGGTAAACAGCCTAGACTTGGTCA Conservative 44.2%; 0; Score 91.8; DB 8; Pred. No. 1.8e-07; Mismatches 767; Indels 25; Gaps 1956 1896 1836 1417 1086 1026 2016 1146 906 726 666 909 5

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Search completed: March 15, 2005, 10:51:21 Job time : 1109.24 secs

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ALIGNMENTS

REFERENCE AUTHORS TITLE RESULT 1 CNS00EVL/c ORIGIN FEATURES COMMENT SOURCE ORGANISM KEYWORDS DEFINITION VERSION ACCESSION JOURNAL Bource Determination of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. fly), gen AL069706 CNSUDEVL 1101 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit Genoscope.
Direct Submission Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Drosophila melanogaster (fruit fly)
Drosophila melanogaster GSS. Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi AL069706.1 GI:4949849 (bases 1 to 1101) genomic survey sequence. /organism="Drosophila melanogaster" |mol type="genomic DNA" |db xref="taxon:7227" |clone="BACR29B23" /clone_lib="RPCI-98" /note="end : T7" Score 97.8; DB 9; Pred. No. 8.7e-08; seqref@genoscope.cns.fr

Query Match Best Local Similarity

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  Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department (Cancer Genetics at the Roswell Park Cancer Institute in Buffaloo BCORI digestion of Drosophila DNA provided by the BDGP from the
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Ephydroidea; Drosophilidae; Drosophila.

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Mammalia; Eutheria; Rodentia;
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/db zref="taxon:7227"
/clone="BACRO8K10"
/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                  GI:47998186
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Pred. No. 1.1e-07;
1; Mismatches 210
                                                                                                                                                                                                                bp DNA linear (
clone:MSMg01-201G10.TJ,
Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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RESULT 2 CNS0039G/c

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Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abeertc.riken.jp). Tsukuba Institute, please contact Kuniya Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
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R.Site 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1542)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing : TJ
LIBRARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y. BAC end Sequences of Library MSMg01
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AAAACAAATTCAATGAGATAAAATATCTTACAATGAAAAGAAGGACAATGTCTCTTTGAA 1103
                                                                                                                                                                                                            GTACAGGTTAAAACTTTTACAAGAATTTATATTAAACGAAAATCATTTTATAACATGTCT
                            AAAACAAATAGGTACTCCCTCCGTCCCTCTGAAATGTATACATATGGATTGGACACGGAG
                                                                                                                                                CTCGGCTGTCATTATAATAGGGATCACTTACTGATCATCCATTAA-----AACCTTGTT
                                                                                                                                                                                                                                                                      ATAAGAGAGGTTAGTAAACAGAAAGCAGGTAAAAACAAGAGCTTGCTGCTGTGTTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus molossinus"
|mol type="genomic DNA"
|sub_spectes="molossinus"
|db_xref="taxon:57486"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MSMg01-201G10.TJ"
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: EcoRI
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Pred. No. 2.2e-07;
0; Mismatches 523;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                 Web : www.genoscope.cns.fr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BBGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain v2; on bw sp, the same strain used for the BDGP's plant EST libraries. A more detailed description of the library
                                                                                                                                                                                                                        and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
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Best Local Similarity 20.2%; Pred. No. 2.

Matches 173; Conservative 325; Mismatche
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    CL509408 1758 bp
SAIL_811_H11.v3 SAIL Collection
                                                                     WWWMHWWAHWATWW 1037
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                                                                                                          CHMYHDMHMYMYCCHYYCTCHTHATTHYHYMCTCYHYCTWHTYWTAYWWAWTAHAMTTAT
                                                                                                                             TCATCACATCAATÇITAÇAÇCACAAACCTTGAGÇTTAAȚTTŢTCŢACTTAŢŢCTCAGCAA 2036
                                                                                                                                                    ТНМСМСНННМНСТСННННТМҮНМТСНЖМЖНМНЖНЖЖМАТЖМТТМТТММММССММННН
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                                                                                                                                                                                               ТWWHHTTTHWAWWHTHTWCWWWWHATTWTWATHCWACMTWHWHHWMHMHHHHHMACHAHHH
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                                                                                                                                                                                                                                          TGTTTGAACAATGTATGTCCGGTGTACATCTATGACCTTTCAACTCAAACTAGTGAATAA 1799
                                                                                                                                                                                                                                                                                                                                 AWWITHIWWIHAYHWAITHYYYYMYCAMMCMCTHICHHCYYYYHHYTAHHIHTHHHWYAHY
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/note="end : TET3"
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Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Bmail: allen.sessions@syngenta.com
ABRC Stock Number CS836276; T-DNA left border flanking sequences
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
h 4.6%; Score 94.6; DB 9; Similarity 34.2%; Pred. No. 3.3e-07;
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Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Pat Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B., Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A. A high-throughput Arabidopsis reverse genetics system Plant Cell 14 (12), 2985-2994 (2002)
                                           CTGCTGTGTGTTAGTTGTTGTGAGCTCATTTCTTTAAAAGTAATGTAAACTGATCTAAA 914
                                                                                            TTAAGTTACTAATAAATAAGAGAGGGTTAGTAAACAGAAAGCAGGTAAAAACAAGAGCTTG
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/db xref="taxon:3702"
/clone="SAIL_811_H11.v3"
/clone_1ib="SAIL_Collection"
/note="T-DNA left border sequences were isolated using modified TAIL-PCR strategy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis
/mol_type="genomic DNA"
/ecotype="Columbia"
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AATAAANATATTANTTATNTNANAT 1532
                                                                                                                                         TATATUNNTATUTTATA-TTUTATAAATUNTAATANNAATAANTATATATATTATTTUNA
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                                 AACATTGATGTTAGCGTACTATAAAT 1954
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Neodiplogasteridae, Pristionchus.
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Spemannstr. 37-39, Tuebingen
Tel: 00497071601371
Fax: 00497071601498
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Evolutionary Biology
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 AAGAATTTATATTAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAG
                            AAAAGTAATGTAAACTGATCTAAAG-CACATAGAAATTTAGTACAGGTTAAAACTTTTAC
                                                                                      AAAGCAGGTAAAAACAAGAGCTTGCTGCTGTGTGTTTAGTTGTTGAGCTCATTTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Ppa EcoRI BAC Library" /note="The library was generated by a partial digest the genomic DNA with EcoRI and cloning into the BAC vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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TITLE
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AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                               RESULT 7
CC262481/c
                                                                                                                                                                                                                                                                    DEFINITION
 Gallus gallus (chicken)

ISM Gallus gallus

Gallus gallus

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Phasianinae; Gallus.

CE 1 (bases 1 to 1202)

RS Kremtzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,

Warren, W., Graves, T., Mardis, E. and Wilson, R.

Gallus gallus BAC End Reads

Unpublished (2003)

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                        702
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CH261-167M9 Sp6.1 CH261 Gallus g
genomic survey sequence.
CC262481
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Best Local Similarity
Matches 393; Conserv
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ATATGAATAAATCAGTTATCTGAAAAGCAAATAATCTTTGTAAAACAGCGTTCGGTCA 1605
                                                                                                               TATTTATATATAAAAATÄTAAATTÄTAAATTTTÄAÄÄATÄTTTTÄTÄTAAAATTTTAA
                                                                                                                                                                        AAAAAAAATTTATTTTATATTAATATAAATTTATTNTATAAT--
                                                                          AATACTATATTAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTA 1545
                                                                                                                                         GTTATTTTGATTTCATAAGATTATAAATCTATGTTATAATGATAATATAATTTTAAAAAT
                                                                                                                                                                                             АРАТТТАСТАТТТГВАБАДАГТТТВАДАГВТАТАБДАТТВАБТВЕСТАТАДАД 1365
                                                                                                                                                                                                                                                                                     Aaaaaatäattaaaatätätnätaanäätttättättaataaaaätatttätätääaää
                                                                                                                                                                                                                                                                                                              ATGTAGAGTAAAAAGAAAAGAAAAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATAT 1245
                                                                                                                                                                                                                                                                                                                                                                                                    GTCCCTCTGAAATGTATACATATGGATTGGACACGGAGACTAAGAAAAATGTATAAAGTA 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 30
High quality sequence stop: 105.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Westor: pTARBAC2.1; Site 1: EcoRI; Site_2: Eco
CH261 Female Chicken library - For library and clone
ordering information: http://www.chori.org/bacpac"
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/clone_lib="CH261"
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/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-167M9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Gallus gallus"
/mol_type="genomic DNA"
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Pred. No. 6.6e-07;
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SOURCE
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                                                                                                                                                                                                                                                                                        Local Similarity
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR05NI1 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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CANATTCAATGAGATAAAATATCTTACAATGAAAAGAAGGACAATGTCTCTTTGAAAAAA 1107
                                                                                                                                                                   TAGTACAGGTTAAAACTTTTACAAGAATTTATATTAAACGAAAATCATTTTATAACATGT
                                                               CTCTCGGCTGTCATTATAATAGGGATCACTTACTGATCATCCATTAAAAACCTTGTTAAAA 1047
                                                                                                                                   AGTTGTTGTGAGCTCATTTCTTTAAAAGTAATGTAAACTGATCTAAAGCACATAGAAATT
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                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic un
/db_xref="taxon:7227"
/clone="BACR05N11"
                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Drosophila melanogaster"
|mol_type="genomic DNA"
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/note="end : TET3"
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                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                     Score 92.4; DB 9;
Pred. No. 8.5e-07;
5; Mismatches 469;
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survey sequence TET3 end of BAC #
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AL069706.1
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Drosophila melanogaster
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1108 CAAATAGGTACTCCCTCCGTCCCTCTGAAATGTATACATATGGATTGGACACGGAGACTA 1167
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP)
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department
                                                                                                                                                                                                                                                             Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence T7 end of B
BACR29B23 of RPCI-98 library from Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGTTCACGGGCATCATTGAGCAGCACTAGACTGTTTGAACAAT 1751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAWTGKGAATGKKKKGKTARKKKGRKGTTAARAATDGTAAGAKRATAAKKTKTKAATKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pterygota;
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FEATURES

source

Matches 197; Query Match Best Local

Local

Similarity

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1250 GATAGATTTAGAAAAGTAGTTGAAAGTAGTGGGTGGGGTGTGGATTTTTATATATATAAAAAT
                                                      ISB1-72J8 T7.1 ISB1 Xenopus tropicalis genomic genomic survey sequence.
CL118721
CL118721.1 GI:40612356
GSS.
                  Xenopus tropicalis (western clawed Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                TTTGTTTCAGAAATTAAAATAAATTAT 1697
                                                                                                                                                                                                                                                                                                                    AWAWWIWATATIWITATIAAAWIWIATIWATIWATIWAWIWIATAWITIWIATATAT
                                                                                                                                                                                                                                                                                                                                                    ATWWTAWTAWATATATTTATTAAWWTAT 1020
                                                                                                                                                                                                                                                                                                                                                                                          GAATAAATCAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATG 1609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29B23"
/clone_"BACR29B23"
/clone_lib="RPCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine Email: submissions@watson.wustl.edu Insert Length: 75000 Std Error: 0.00 Seq primer: T7 TAATACGACTCACTATAGGG Class: BAC ends
GAAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGAAAGTGTATAGAATT 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

1 (Dases I to 1608)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2003)
Contact: Richard K Wilson
                                    АТВАВАВАВАТВАВАВТВАВАВАТТВАВАВАВАТАТЯТВАВАВАТВАВАВАТВАВАВА
                                                                                                                                                AAGAGAAAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATATAATTGATAGATTTAGA 1261
                                                                                                                                                                                        TACATATGGATTGGACACGGAGACTAAGAAAATGTATAAAGTAATGTAGAGTAAAAGA 1201
                                                                                                                                                                                                                                                                AGAAGGACAATGTCTCTTTGAAAAAACAAATAGGTACTCCCCTCCGTCCCTCTGAAATGTA 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                   TAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACT 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTTGCTGCTGTGTTTAGTTGTTGTGAGCTCATTTCTTTAAAAGTAATGTAAAC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u> АТАРАТТАРАРТАТАРАРАРАРАРАРАРАРАРАТАРАДАТАРАРАРАТАТАРАРАРАД</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="ISB1"
/note="Vector: pBeloBAC11;
Library Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
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0; Mismatches
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Gaps

397

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ACCESSION VERSION KEYWORDS

SOURCE

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ORGANISM

RESULT 10 CL118721 LOCUS

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REFERENCE
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                                                                                                                                                                                                                                                                                                    National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapba-r@mail.nih.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
cDNA Library Preparation: Gina Zastrow-Hayes
cDNA Library Preparation: Gina Zastrow-Hayes
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1067)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: NDKW74 row: e column: 02
High quality sequence start: 8
High quality sequence stop: 462.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1067 bp mRNA linear EST 30-WAY-2003
AGENCOURT_14286445 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
CD386564
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Daniela S. Gerhard,
Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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                                               /clone_lib="NIH_MGC_173"
/note="Vector: pDONR201, MSTHOD - full-length enriched;
LJBR PRIMING - oligo dT; MSTHOD - full-length enriched;
LJBR PROVIDER - Bradfield"
                                                                                                                         /tissue_type="embryonic trophoblasts,
cells"
                                                                                                          /lab_host="DH10B TonA"
                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                    .1067
                                                                                                                                                       xref="taxon:9606"
                                                                                                                                                                      type="mRNA"
    .3%;
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    88.8;
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                                                                                                                                                                                                                               sequence.
AG347098
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                                                                                                                                                                                                  AG347098.1
GSS.
                                                                          Unpublished
                                                                                          Hattori,M., Toyoda,A., Noguchi,H., BAC end Sequences of Library MSMg01
                                                                                                                                                                      Mus
                                                                                                                                                                                  Mue
                                                                                                                                                                                                                                                              Mus musculus molossinus
                                             Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                 musculus molossinus
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DNA,
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clone:MSMg01-142102.T7,
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genomic survey
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        1567 GAAAAGCAAAT---AATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATGTGT
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R.Site 2
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Similarity 45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, J. (E-mail:hattori@gsc.riken.jp, URL:http://hgp.9sc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Phone: 81-298-36-9199
                                         AGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATGAATAAATCAGTTATCT 1566
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LIBRARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATGTCTCTTTGAAAAACAAATAGGTACTCCCTCCGTCCCTCTGAAAT----GTATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAAAAGAAGGAC
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/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
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/clone_lib="MSMg01 Mouse Male BAC Library"
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/sex="male"
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Pred. No. 3.9e-06;
0; Mismatches 551
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                                                                                                                                                                                                                                                   Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                               Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   615
                                                                                                                                                                                                                                                Fax: 00497071601498
                                                                                                                                                                                                                                                                                                                             Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1392)
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P052-4-C08.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pristionchus pacificus
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                                                                                                                                                                                                                  BAC ends.
                                                                                                                                                                                                                         ralf.sommer@tuebingen.mpg
                                                     /db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
                                                                                                                          /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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                                 GAAAGTGTATAGAATTAAATGGGACAGAGGGAGTAATACCTTTATGATATATAAATTTTT
                                                                                                                                       AAATTTACTATTTTGAGAAAGTTTTGAAAATGTATAGAATTGAGTGGGACATCCATAAAAG 1365
                                                                                                                                                                                AGAGTAAAAAGAAAAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATAATT 1249
                                                                                                                                                                                                                                               GGATCACTTACTGATCATCCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATAT 1069
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                                                                          CTCTGAAATGTATACATATGGATTGGACACGGAGACTAAGAAAAATGTATAAAGTAATGT 1189
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Kremitzki,C., Higginbotham,J., Warren,W., Graves,T., Mardis,E.
Gallus gallus BAC End Reads
Unpublished (2003)
Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                  High quality sequence start: 24 High quality sequence stop: 85.
                                                                                                                                                                                                                                                                                                                                                     Seq primer: RM1 TACGACTCACTATAGGGAGA
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CH261-180N11_RM1.1 CH261 Gallus
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                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 182000
                                                                                                                                                                                                                                                                                                                                                                            Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
              Conservative
                                                                                                                                                                                                                                                                   /organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                               /clone="CH261-180N11"
/sex="female"
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                  4.3%;
                                                                                                                                                  Score 88; DB 8;
Pred. No. 5.4e-06;
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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GAGACTTAGGTCAAAAATGGACGCTGGTAAACAGCCTAGACTTGGTCACTGATAAATAGA 738
                                                                                                                        GTTTGTTAATATATATGTTTACACTTACAAGAGGATATTCGTAATACTTTTAGACGACAA 678
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                                          ATATGAATAAATCAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCA 1605
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/clone_lib="CH261"
/clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female_Chicken library - for library and clone ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                      0; Mismatches 600;
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genomic clone
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e CH261-180N11,
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Sakaki, Y.

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                                                            1696 bp DNA TIMES. DNA, clone:MSMg01-142C12.T7,
                                                                 GSS 02-JUN-2004, genomic survey
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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Lirect Submission.

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                           991
                                                                                                                                                                                                                                                                                                                                                                              955
                                                                                                                                                                                                                                                                                                                                              775 АТТААЛАТТАGAGCTATTAATTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         464;
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R.Site 2
                              ACTTACTGATCATCCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTAC 1074
                                                                                                                          ATCATATTAAAATAATATCTATCAATAATAAACNTACAAACATAATATAAAATATCACC
                                                                                                                                                        TTTATATATAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATC
                                                                                                                                                                                       4.3%;
Similarity 47.3%;
                                                              GTAATGTAAACTGATCTAAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAA 954
                                                                                                                                                                                                                                                     CAGGTAAAAACAAGAGCTTGCTGCTGTGTTTTAGTTGTTGTGAGCTCATTTCTTTAAAA 894
                                                                                                                                                                                                                                                                                                                 Sequencing : T7
LIBRARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                          TAGACTTGGTCACTGATAAATAGATAATTGTTAGTATAATATAGTAGGATCTACAATGAC 774
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Mus musculus molossinus
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hattori,M., Toyoda,A., Noguchi,H., Kojima,T.
BAC end Sequences of Library MSMg01
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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- AATAAAAACAATATATATATATATATATATAAAATAACAAATACAATATATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus mo:
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-142C12.T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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Pred. No. 5.4e-06;
0; Mismatches 501
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Sciurognathi; Muridae; Murinae; Mus
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Search completed: March 15, 2005, 15:16:41 Job time: 6535.36 secs
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Maximum Match 100%
Listing first 45 summaries
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Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

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11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

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13: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

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19: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

21: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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10331.389 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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70.6 70	75 71	83 79.4	88.6	91.6	91.8	93	99.4	Score
3 3 4 4	3.7	3.9	4.3	4.5	4.5			Query
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13 US-10-312-841-1 13 US-10-027-632-113786	US-10-240-453-206 US-10-311-455-490	17 US-10-211-179-11 18 US-10-719-993-6854	US-10-473-126-240	US-10-473-126-386	US-10-473-126-240	US-10-312-841-1	18 US-10-473-126-386	ID
Sequence 1, Appli Sequence 113786,	Sequence 206, App Sequence 490, App	GENERAL INFORMATI Sequence 6854, Ap	Sequence 240, App	Sequence 386, App	Sequence 240, App	Sequence 1, Appli	Sequence 386, App	Description

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US-10-027-632-113786	US-10-027-632-113788	-10-027-632	US-10-027-632-113786	US-10-473-126-328	US-10-311-455-1676	US-10-221-714A-461	US-10-311-455-394	US-09-960-352-11234	US-10-278-698-769	US-10-278-698-255	US-10-027-632-97533	US-10-027-632-97533	US-10-723-860-7676	US-10-311-455-1128	US-10-311-455-228	US-10-311-455-1115	US-10-311-455-1984	US-10-433-793-24	US-10-240-453-107	US-10-239-676-95	US-10-257-166-17	US-10-311-455-191	US-10-311-455-2128	US-10-741-600-17905	US-10-741-601-5746	US-10-312-841-2	US-10-257-166-120	US-10-221-613-195	-632	US-10-027-632-113787	US-10-027-632-113786	US-10-027-632-113788	CC +0 000 ++0.00
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113786,	113788,	113787,	113786,		٥	461, App			769, App	255, Api	97533, A	•	7676, Ap	•		1115, Ap					17, Appl	191, App	2128, Ap	17905, A	5746, A	: 2, App.	120, App	195, App	113788,	113787,	113786,	113788,	1 1 1 1 1 1

ALIGNMENTS

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668 TTAGACGACAAGAGACTTAGGTCAAAAATGGACGCTGGTAAACAGCCTAGACTTGGTCAC 727	2035 ATTTTAAATATTTTTAATTTTTAAAAAAATTTTATTAAAA	608 CCGTTTAACCAGTTTGTTAATATATATGTTTACACTTACAAGAGGATATTCGTAATACTT 667	1975 ATTAATATTAATTTTAATTTTAAAATTTAAAAATTTTAAATAT	548 ATGCTTCTCAAAATGTTTTTTATATGTAAAATAATGCCCATCCAAGGATAAGTAAAATTC 607	vative (Query Match 4.8%; Score 99.4; DB 18; Length 8056;	; OTHER INFORMATION: chemically treated genomic DNA (Homo mapienm) US-10-473-126-386	FEATURE:	ORGANISM: Artificial Sequence	TYPE: DNA	SEQ ID NO 386	Q ID NOS:	CURRENT FILING DATE: 2003-09-26	FILE REFERENCE: CURRENT APPLICATION NUMBER: US/10/473,126	TITLE OF INVENTION: proliferative disorders	TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell	ics AG	GENERAL INFORMATION:	Sequence 386, Application US/10473126	RESULT 1 US-10-473-126-386	
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TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des I
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des I
TITLE OF INVENTION: US/10/312,841
CURRENT APPLICATION UNUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 3673778
TYPE: DNA
ORGANISN: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
FEATURE:
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Best Local Similarity 43.8%;
Matches 587; Conservative
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Publication No. US20030186277A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (3294164)
                               1714246 АТАГАДААТАТАТАЛАЛАТАТАТАЛАЛАТАТАТАТАЛАЛАТАТАТАЛАЛАТАТАТАЛА
                                                                                                      1714305
                                                                                                                                                          1714365 ААААТАТАТАТАТАААТАТАТАТАТАЛАААТАТАТАЛААТАТАТАТАЛАААТАТАТАТАЛАА
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AACAAATTCAATGAGATAAAATATCT-TACAATGAAAAGAAGGACAATGTCTCTTTGAAA 1104
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Pred. No. 1.2e-05;
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RESULT 3
US-10-473-126-240
US-10-473-126-240
Sequence 240, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
ITITLE OF INVENTION: Methods and nucleic acids for ITITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: chemically treated
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US-10-473-126-386/c
US-10-473-126-386/c
; Sequence 386, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids
; TITLE OF INVENTION: proliferative disorders
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CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 386
LENGTH: 8056
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA
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                                       Sequence 240, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
ITITLE OF INVENTION: Methods and nucleic acids for the analysis of
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 240
LENGTH: 8056
TYPE: DNA
CECANITY
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US-10-473-126-240/c
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   FEATURE:
OTHER INFORMATION: chemically
                         ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                      ТТА́ВА́ВАЯТТТСЯТА́ТА́ВА́ВАВСАТВВВАВТА́ВВАВСВАТВВВВТВТВВВТВВТВВВВВВТ
                                                                                                                                                                                                                                                                                                            GAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATGTGTATT 1626
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Best Local Similarity 45.4%;
Matches 442; Conservative
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                                                                                              TCGATTACCGCCTTTTATAA-----TTTTACAATACTGAGTAATATGAATAAATCAGTTA 156:
                                                                                                                              TAAATCTATGTTATAATGATAATATAATTTTAAAAATAATACTATATTAATTCTGATTAG
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TTAAAAAAATAA 427
             TTAAAATAAATTA 1696
                           ACACGGAGACTAAGAAAAATGTATAAAGTAATGTAGAGTAAAAAAGAAAAGAAAAGAAAAG
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                                                                                       TTAATTTTAAATTTTCGAATATCGAAAAAAATATTAAAAAACGAATATATAACGTTTTAA
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Pred. No. 9e-06;
0; Mismatches 519;
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RESULT 6
US-10-211-179-11
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF PHC
FILE REFERENCE: PTS-0011
CURRENT APPLICATION NUMBER: US/10/211,179
CURRENT FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 119
OTHER INFORMATION: n = a, t, c, or g
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Best Local Similarity 46.0%;
Matches 458; Conservative
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ATAATACTATATTAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTTACAATACTGAG 1543
                                                                                                                                                              GAAAGTGTATAGAATTAAATGGGACAGAGGGAGTA-ATACCTTTATGATATATAAATTTT
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                                                                                                                                 Score 83; DB 17; Length 158001; Pred. No. 0.00025; 0; Mismatches 530; Indels 7;
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Sequence 6854, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC FOLYMORPHISMS ASS
TITLE OF INVENTION: ALTHEIMER'S DISEASE, MET
FILE REFERENCE: CL001496
CURRENT APPLICATION UNMEER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6854
LENGTH: 74665
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US-10-719-993-6854
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US-10-719-993-6854
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Best Local Similarity 44.8%;
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                                           ACTCCCTCCGTCCCTCTGAAATGTATACATATGGATTGGACACGGAGACTAAGAAAAATG 1176
                                                                              tatgttääätatatttätätatgtäätätgtäatätattacataatätätttätätätgt
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APPLICANT: OLEK, Alexander
APPLICANT: PIEBENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Disgnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: by Means of Assessing the Methylation Status of
TITLE OF INVENTION: With DNA TRanscription
FILE REFERENCE: 5013.1009
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: DCT/EP01/03973
PRIOR APPLICATION DATE: 2001-04-06
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                                                                                                                                                                                                                                      Sequence 206, Application US/10240453
Publication No. US20030148326A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       СТТТСААСТСАААСТАСТВАТААТВАТССТАСТСТВС-ААТАСАТСТТТТСАААТТТСААСАА 1834
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 206
LENGTH: 11745
TYPE: DNA
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Best Local Sin
Matches 499;
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NAME/KEY: unsure
LOCATION: (9105)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
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                                                                                                                                           ATTTACTATTTTGAGAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGA 1367
                                                                                                                                                                                                                                         ATAACATAAAAAAAAACCTTTCAAAACAATAAAAATA--ATCAATTATCATATATACT 4331
                                                                                                                                                                                                                                                               GTAGAGTAAAAAGAAAGAGAAAAGAAAAGTGGGGTAAAGTAGCGGGGACCCACCAATATATAA
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TTTTCTTTAAATAAATAATATTAAAAACAACTCTATATATCAATAAAAATAACCCAAAATAA
                     TACTATATTAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAAT
                                              TATTTTGATTTCATAAGATTATAAATCTATGTTATAATGATAATATTAATAATAATAA
                                                                                             АТТАЛАЛАЛАТАЛАЛАТАЛТАЛАТАЛАЛАСАЛСАЛАТАТАЛАСАЛСТАТТАТАЛАЛАЛ 4151
                                                                                                                    AAGTGTATAGAATTAAATGGGACAGAGGGAGTAATACCTTTATGATATATAAATTTTTGT
                                                                                                                                                                                           TTTÄÄÄTCCTÄÄÄÄÄACÄÄÄÄÄCTAÄÄÄÄTCÄTTTAATTATCÄÄTÄTÄTÄACTCÄÄTÄÄT 4271
                                                                                                                                                                                                                 ACCABABACABABACTABATCACTCTBACATTTBABABATCTBATBABABACABABABACA 4449
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Pred. No. 0.0027;
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Best Local Similarity
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US-10-311-455-490/c
; Sequence 490, Application US/10311455
; Publication No. US20030143606A1
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                                                                                                                                                                                                                                                                     TGTAATATTTATCAACACCTCAACATTGA 1936
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Associated with the Immune System by
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TITLE OF INVENTION: Cytosine methylation
FILL REFERENCE: 5013.1014
CURRENT APPLICATION UNMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION UNMBER: PCT/EP01/07537
PRIOR APPLICATION UNMBER: DE 10032529.7
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 490
LENGTH: 5930
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
CTUEN INVESTMENT OF SEG ID NOS: 2424
CREATURE: THE ORGANISM: Artificial Sequence ; OTHER INFORMATION: chemically treated US-10-311-455-490 **ААТТАЛАЛАЛАЛАЛАЛАТАТАТАЛАЛАЛАСАТТТАСТАСТТТАЛАТАТТТАТАЛАСААТ** 5095 AATGTAAACTGATCTAAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAATT СТААТТТАТААТАТТТСААЛАСААТАТТАЛАЛТАЛАЛСЛАЛЛАТАСЛАЛАТТАЛАТАЛЛА TATATTAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCAC 1016 TTACTGATCATCCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAA 1076 0; Score 71; DB 15; I Pred. No. 0.011; 0; Mismatches 420; genomic DNA Length 5930; (Homo sapiens) Indels 8 Gaps 4975 956 4

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US-10-312-841-1
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                                                       Query Match 3.4%;
Best Local Similarity 42.2%;
Matches 644; Conservative
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TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des
FILB REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
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Publication No. US20030186277A1
GENERAL INFORMATION:
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                                                                                                                                                                 NAME/KEY: unsure
LOCATION: (3294164)
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OTHER INFORMATION:
                                                                                                                                                                                                                 FEATURE:
1435
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Pred. No. 0.12;
0; Mismatches 874;
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1225 TAGCGGGACCCACCATATATAATTGATAGATTAGAAAAGTAGTTGAAAGTAGTGGGTG 1284
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US-10-027-632-113786
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US-10-027-632-113786/c
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PRIOR PILING DATE: 2000-07-12
PRIOR PPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
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SOPTWARE: FastSEQ for
SEQ ID NO 113786
LENGTH: 3252
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                                                                                              Matches 474;
                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.1.29
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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 GACTTAGGTCAAAAATGGACGCTGGTAAACAGCCTAGACTTGGTCACTGATAAATAGATA 740
                                 TTAATACTAACAATTTTTATACTTATATTAATGAGTTTAATATGTTTATACTGTAATATA
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                                                                                         Score 70; DB 13; Length 3252;
Pred. No. 0.014;
0; Mismatches 600; Indels 1
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113787
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-33
PRIOR FILING DATE: 1999-11-33
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/167,363
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; Sequence 113787, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
GENERAL INFORMATION: David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
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Best Local Similarity 43.6%;
Matches 474; Conservative
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 113787
LENGTH: 3252
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                                                AATATTTATATATATATATATTAATAAAAACAATATATATATATATATTTAATATATACAATATT 1775
                                                                                                                                                 CCATTAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAAAAGAAGG 1087
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Pred. No. 0.014;
0; Mismatches 600; Indels 1
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             ; ORGANISM: Human US-10-027-632-113788
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US-10-027-632-113788/c
; Sequence 113788, Application US/10027632
; Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PRILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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                                                                                                         PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOPTWARE: FastSEQ for Windows Version 4
SEQ ID NO 111788
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
                                                                        TYPE: D
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Query Match
Best Local Similarity
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TTATATAATATAATATATTATTCATATATTTATATATTTTAATATGTTTAACTATA
                                                                                                                 AGTCGATTACCGCCTTTTATAATTTTTACAATACTGAGTAATATGAATAATCAGTTATCT
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                                                                                                                                                                                                                                                            GACAGAGGGGAGTAATACCTTTATGATATATAAATTTTTTGTTATTTTGATTTCATAAGATT
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                                                             GAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATGTGTATT 1626
                                                                                              TTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGAAAGTGTATAGAATTAAATGG
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Pred. No. 0.014;
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Best Local S
Matches 474
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 113786
LENGTH: 3252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Local Similarity 43.6%;
hes 474; Conservative
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                 AMANTCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACTGATCAT 1027
                                                                                                                                                                                                                                                                                                           GACTTAGGTCANAAATGGACGCTGGTAAACAGCCTAGACTTGGTCACTGATAAATAGATA 740
                                                                                                              TCTAAAGCACATAGAAATTTAGTACAGGTTA-AAACTTTTACAAGAATTTATATTAAACG 967
                                                                                                                                              AGCTTGCTGCTGTGTTTAGTTGTTGTGAGCTCATTTCTTTAAAAGTAATGTAAACTGA 908
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US-10-027-632-113787/c

i Sequence 113787, Application US/10027632

i Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

ITILE OF INVENTION: Identification and Mappi
ITILE OF INVENTION: Polymorphisms in the Hu
CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR APPLICATION NUMBER: US/0/218,006

PRIOR APPLICATION NUMBER: US 60/18,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/156,358

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; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 113787
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113787
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                      ATAPATCTATGATTATGATA-ATATAATTTTAAAAATAATACTATATTAATTCTGATT
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Maximum Match 100%
Listing first 45 summaries
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        45554873 segs, 20411521753 residues
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Gapop 10.0 , Gapext 1.0
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| Cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*
| Cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq:*
| Cgn2_6/ptodata/1/pna/US06_COMB.seq:*
| Cgn2_6/ptodata/1/pna/US07_COMB.seq:*
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Pred. No. is the score greater to and is derived be
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2 35 US-09-806-197-7
6 35 US-09-806-197-7
8 35 US-09-806-197-7
8 35 US-09-806-197-3
8 35 US-09-806-197-3
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7 41 US-09-949-003C-4601
7 40 US-10-90-774-1594
6 US-10-940-774-1594
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8 US-60-207-905-23
8 US-60-208-837-28
6 US-10-266-090-24327
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                                                                   ALIGNMENTS
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                                                                                                                                                                        Sequence 1, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 1, Appli
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Sequence 18474, Appli
Sequence 240, App
Sequence 240, App
Sequence 240, App
Sequence 643, App
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Sequence 12776, Ap
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Sequence 28654, Ap
Sequence 27, Appl
Sequence 28, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 27, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 27, Appl
Sequence 28, Appl
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GENERAL INFORMATION:
APPLICANT: NISHIKAWA, SATOMI
APPLICANT: OEDA, KENJI
TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TERMINATORS
FILE REFERENCE: 7372-70911
CURRENT APPLICATION NUMBER: US/09/806,197
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 29
SOPTWARE: Patentin Ver. 2.1
ENGTH: 2052
TYPE: DNA
ORGANISM: Daucus carota
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; GENERAL INFORMATION:
; APPLICANT: NISHIKAWA, SATOMI
; APPLICANT: OEDA, KENJI
; TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TER
; FILE REFERENCE: 7372-70911
; CURRENT APPLICATION NUMBER: US/09/806,197
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: Daucus carota
US-09-806-197-7
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RESULT 3
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; Sequence 5, Application US/09806197
; Sequence 5, Application US/09806197
; GENERAL INFORMATION:
; APPLICANT: NIGHIKAWA, SATOMI
; APPLICANT: NEHIKAWA, SATOMI
; TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TERMINATORS
; FILE REFERENCE: 7372-70911
; CURRENT APPLICATION NUMBER: US/09/806,197
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2056
; TYPE: DNA
; ORGANISM: Daucus carota
US-09-806-197-5
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                                                                           APPLICANT: NISHIKAWA, SATOMI
APPLICANT: OEDA, KENJI
ITITLE OF INVENTION: PLANT PROMOTERS AND PLANT TEI
FILE REFERENCE: 7372-70911
CURRENT APPLICATION NUMBER: US/09/806,197
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 2048
TYPE: DNA
ORGANISM: Daucus carota
US-09-806-197-3
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Sequence 3, Application US/09806197

; GENERAL INFORMATION:
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; APPLICANT: OEDA, KENJI
; TITLE OF INVENTION: PLANT PROMOTERS AND PLANT TERMINATORS
; FILE REFERENCE: 7372-70911
; CURRENT APPLICATION UNMBER: US/09/806,197
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PATENTIN VET: 2.1
; SEQ ID NO 4
; LENGTH: 2048
; TYPE: DNA
; ORGANISM: Daucus carota
US-09-806-197-4
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; NAME/KEY:
; LOCATION:
US-09-300-487-2
                                                                                                                      Query Match
Best Local Similarity
Matches 367; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
2042 hase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09300487
GENERAL INFORMATION:
APPLICANT: TORIKAI, Satomi
APPLICANT: OEDA, Kenji
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stewart, Raymond C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)205-8000
                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                      MOLECULE TYPE: DI
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 12-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PLANT PROMOTER AND UTILIZATION NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         ORGANISM: Daucus ca
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                           LENGTH: 2042 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                       ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
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ZIP: 22040
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CITY: FALLS CHURCH
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                    1610 GGAAGTTCATGTGTATTCAATAGTTTAATATAAAGTAAAGTTAAATTTAAATTGTTATT
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CCAAGTTCACGTGTATTCTAAAATGTTAATACTAACATGAGTATTTTCTT--TTCAAGGT
                                                      AAATTATTTATCTGAATGATAACATCTTTGTAAACAAAACTGGGCCAAATAGGACCATAA 1602
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                                                                                                                Score 241.2; DB 20; Length Pred. No. 7e-31; 0; Mismatches 128; Indels
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                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 base pairs
TYPE nucleic acid
ORIGINAL SOURCE:
               MOLECULE TYPE: DI
HYPOTHETICAL: NO
                                                                                                                                                                        NAME: Stewart, Raymond C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 21/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)205-8000
                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 12-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TORIKAI, Satomi
APPLICANT: OEDA, Kenji
TITLE OF INVENTION: PLANT
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                                                     STRANDEDNESS:
TOPOLOGY: lir
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T: P.O. BOX 747
PALLS CHURCH:
VIRGINIA
RY: UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703)205-8050
                                                     linear
                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kenji
N: PLANT PROMOTER AND UTILIZATION THEREOF
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US-10-473-126-386
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GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 386
LENGTH: 8056
TYPE: DNA
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Best Local Similarity 89.6%;
Matches 223; Conservative
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                                                                                                                                                                                                                                                          Matches 624;
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                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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CTATTAATTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAGCAGGTAAAAACAA
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                                          TTAGACGACAAGACTTAGGTCAAAAATGGACGCTGGTAAACAGCCTAGACTTGGTCAC
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ISOLATE: Kurc
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44.5%; Pred. No. 1.2e-06;
ative 0; Mismatches 761;
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  GAGCTTGCTGCTGTGTTAGTTGTTGTGAGCTCATTTC----TTTAAAAGTAATGT
                                                                                 AATTTTAAATAATAATATTTTAATAAAAATTTTGTTGTTTGAATTGTAAATAAAATTTT
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                                                      ---TTTGAACAATGTATGTCCGGTGTACATCTATGACCTTTCAACTCAAACTAGTGAATA 1798
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APPLICANT: WANG, RONG-LIN

TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE

TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES

FILE REFERENCE: NADII.058C1

CURRENT APPLICATION NUMBER: US/10/266,090

CURRENT FILING DATE: 2002-10-03

PRIOR APPLICATION NUMBER: US 10/260,703

PRIOR FILING DATE: 2002-09-26

PRIOR FILING DATE: 2002-09-26

PRIOR APPLICATION NUMBER: US 60/326,117
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; NAME/KEY: misc feature
; LOCATION: (1)...(1069)
; OTHER INFORMATION: n = A,T,C
US-10-266-090-13474
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US-10-266-090-13474
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NUMBER OF SEQ ID NOS: 51812

SOFTWARE: FBSESEQ for Windows Version 4.0

SEQ ID NO 13474

LENGTH: 1069
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Best Local (
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APPLICANT: BONA
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ORGANISM: HORDEUM VULGARE
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1323 AAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGAAAGTGTATAGAATTA 1382
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                                         AGAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATATAATTGATAGATTTAGAA 1262
                                                                                                                                                                           АСАТАТСБАТТСБАССАССБАСАСТААБААЛАТСТАТААЛСТААТСТАБАСТАДАЛАДАДА 1202
                                                                                                                                                    AAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACTG 1022
                                                                                                                                                                                                                                                            АТСАТССАТТАЛАДАССТТСТТАЛАДАСАЛАТТСАДТСЯДСАТАЛАДАТАТСТТАСДАТСАДАД 1082
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Pred. No. 3.6e-06;
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US-10-473-126-240
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CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 240
LENGTH: 8056
TYPE: DNA
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TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
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                                                                                                   TAATTTTAATATTTTAAAAAATCGAÄÄTÄAACGAATCGTAAAATTAAAAAAATTTATTTT 1657
                                                                                                                                                     CTGATAAATAGATAATTGTTAGTATAATATAGTAGGATCTACAATGACATTAAAATTAGA 786
                                                                                                                           GCTAȚTAATTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAGCAGGTAAAAACA 846
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                       TTGTAATATTTATCAACACCTCAACATTGATGTTAGCGT 1945
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                                              AATAATTTAAAAAAAAAAAATAAAAAAACGTTAAAATTTAAAAATTTTAAAAATAATAA
                                                                                                                        AACTAGTGAATAATGCATTCTAGAATACATCTTTTCAAATTTCAACAACACAGCTTTAA
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RESULT 11 US-10-473-126-386/c ; Sequence 386, Application US/10473126 중 유

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GENERAL INFORMATION:
APPLICANT: Epigenomics AG
ITITLE OF INVENTION: Methods and nucleic acids for ITITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 386
LENGTH: 8056
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Best Local Similarity
Matches 455; Conserv
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ORGANISM: Artificial Sequence
FEATURE:
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                                                 AATCTATGTTATAATGATAATATAATTTTAAAAATAATACT----ATATTAATTCTGATT
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RESULT 13
US-10-473-126-240/c
; Sequence 240, Application US/10473126
; GENERAL INFORMATION:
, APPLICANT: Epigenomics AG
, TITLE OF INVENTION: Methods and nucleic acids for the analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-806-197-2/c
Sequence 2, Application US/09806197
SERREAL INFORMATION:
APPLICANT: NISHIKAWA, SATOMI
APPLICANT: OEDA, KENJI
TITLE OF INVENTION: PLANT PROMOTERS AND PLANT FILE REFERENCE: 7372-70911
CURRENT APPLICATION NUMBER: US/09/806,197
UMBER OF SEQ ID NOS: 29
SCHWARDER: DESCRIPTION OF SEQ ID NOS: 29
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; SEQ ID NO 2
; LENGTH: 851
; TYPE: DNA
; ORGANISM: Daucus carota
US-09-806-197-2
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Pred. No. 5.4e-05;
0; Mismatches 119;
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CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 240
LENGTH: 8056
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                             TCGATTACCGCCTTTTATAA-----TTTTACAATACTGAGTAATAGAATAAATCAGTTA 1563
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Pred. No. 8.3e-05;
0; Mismatches 519;
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US-10-211-179-11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nicholas M. Dean
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: PTS-0011
CURRENT APPLICATION NUMBER: US/10/211,179
CURRENT FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 119
OTHER IMPORMATION: n = a, t, c, or g
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                                                                                                                                                                                                                                                                                                                                                                                                    TTTAAAAGTAATGTAAACTGATCTAAAGCACATAGA-AATTTAGTACAGGTTAAAACTTT
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                             AAATTTACTATTTTGAGAAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAG
                                                                ATGTAGAGTAAAAAGAAAGAGAAAAGAAAAGTGGGTAAAGTAGCGGGACCCACCAATATAT 1245
                                                                                                                                                                                                  TACAAGAATTTATATTAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAA 1006
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Pred. No. 0.0013;
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; ORGANISM: Human
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(464387)
; OTHER INFORMATION: n = A,T,C or G
US-09-948-941-643
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US-09-948-941-643/c
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CANCER, METHODS OF DETECTION AND U
FILE REFERENCE: CL000788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 12618
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 643
                                                                                                                                                                                                                                                                                                                                Query Match 4.0%;
Best Local Similarity 44.2%;
Matches 523; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/948,941
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,328
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 464387
                                                                                                                                                                                                                                                                 127673
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 TAATTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAGCAGGTAAAAACAAGAGC 851
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                             TCATTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACTGATCATCCAT 1031
                                                                AAAGCACATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAATTTATATTTAAACGAAAA 971
                                                                                                                                                                TTGCTGCTGTGTTTAGTTGTGTGAGCTCATTTCTTTAAAAGTAATGTAAACTGATCT
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                                                                                                                                                                                                                                                                                                                                  Score 81.6; DB 41;
Pred. No. 0.0028;
0; Mismatches 649;
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358687	358747	1804	358807	1744	358867	358927	1624	358987	1567	359047	1511	359107	1451	359167	1391	359227	1332	359287	1272	359347	1212	359407	11	359467	10	359527	10
1994 CUTITITIAAATTATAAATAAAAAAATTAT 1907 		4 TTCTAGAATACATCTTTTCAAATTTCAACAAACAACAGCTTTAACTTTTCTTTC		TGAACAATGTATGTCCGGTGTACATCTATGACCTTTCAACTCAAACTAGTGAATGAA	7 ATTATATATATATATATATATATATATATTATATATAT		ATTCAATAGTTTTAAAAAGTAAAAGTTAAATTAATTGTTATTTTGTTTCAGAAAT		GAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAAAGGGAAGTTCATCATCT	TTATATTATATTATATACAATATTATATTATTATTATTAT	GATTACCGCCTTTTATAATTTTACAATACTGAGTAATATGAATAAATCAGTTATCT 1866		AATCTATGTTATAATGATAATATAATTTTAAAAATAATACTATATTAATTCTGATTACTC		AGAGGGAGTAATACCTTTATGATATATAAATTTTTGTTATTTTGATTTCATAAGATTTAT		AAATGTATAGAATTGAGTGGGACATCCATAAAAGGA-AAGTGTATAGAATTAAATGGGAC	ATATTATATAAAATATACATTATATATAAAAATATATAT	AAAGTAGTGGGTGGGATTTTTATATATAAAAATTTACTATTTTGAGAAAGTTTTG	AAATATACATTATATAAAAATATATATATATATAAAATATACATTATATATAAAAAA	AAAGTGGGTAAAGTAGCGGGACCCACCAATATATAATTGATAGATTTAGAAAAGTAGTTG	TTTATTATATATAAAATATATATATATATATATATATATA		TTTATTATATAAAATATATATATATATATTATATATAT	1092 TGTCTCTTTGAAAAAACAAATAGGTACTCCCTTCCGTCCCTCTGAAATGTATACATATGGA 1161	TTATTATATAAGAATATATAATATATATATATATATATA	1032 TAAAACCTTGTTAAAACAAATTCAATGAGATAAAATATCTTACAATGAAAAGAAGGACAA 1091

Search completed: March 15, 2005, 17:31:32 Job time: 7607.94 secs

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                      seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
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Match
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        10000000111016101711
    US-60-655-875-31136
US-10-517-441-568
US-10-517-441-568
US-11-033-545-796
US-10-517-441-567
US-10-517-441-567
US-10-517-441-568
US-10-517-441-568
US-10-517-441-568
US-10-517-441-568
US-10-932-182h-166179
US-10-932-182h-166179
US-10-517-441-293
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US-10-517-441-293
US-10-517-441-567
US-10-655-875-30892
US-60-655-875-31280
US-60-655-875-1264
US-60-655-875-1264
US-60-655-875-1264
US-60-655-875-21034
US-10-517-441-522
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Sequence 31136, A Sequence 568, App Sequence 568, App Sequence 293, App Sequence 567, App Sequence 568, App Sequence 568, App Sequence 568, App Sequence 568, App Sequence 564, App Sequence 564, App Sequence 567, App Sequence 293, App Sequence 30892, A Sequence 51617, App Se
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946 TTACAAGAATTTATATTAAACGAAAATCATTTATAACATGTC-TCTCGGCTGTCATTAT 1004

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CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR PHILING DATE: 2003-04-17
PRIOR PHILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR APPLICATION UMBER: DE 1030096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
                                                                                                                        APPLICANT: FORKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: MAIR, Sabine
APPLICANT: MAIRR, Sabine
APPLICANT: MAIRR, Sabine
APPLICANT: MAIRR, Sabine
APPLICANT: MANGRICH, Inko
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P
APPLICANT: MARX, Almuth
APPLICANT: MARX, Almuth
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids fo:
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
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US-10-5
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Best Local Similarity 44.6%;
Matches 358; Conservative
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NUMBER OF SEQ ID NOS:
SEQ ID NO 294
LENGTH: 5286
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ORGANISM: Artificial Sequence
FEATURE:
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DS: 2147
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ATCAGTTATCTGAAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGT 1615
                                                                                          TAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTTACAATACTGAGTAATATGAATAA 1555
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Pred. No. 0.00017;
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APPLICANT: HOEFLER, Heinz
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT PILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR PILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR PILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR PILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR PILING DATE: 2003-01-07
PRIOR PILING DATE: 2003-01-01
PRIOR PILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR PILING DATE: 2003-01-01
PRIOR PILING DATE: 2003-01-01
PRIOR PILING DATE: 2003-01-05
PRIOR PILING DATE: 2003-01-05
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Best Local S
Matches 358
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MODEL, Fabian
NIMMRICH, Inko
                                                                                                     TTTAGAAAAGTAGTTGAAAGTAGTGGGTGGGTGTGGGATTTTTATATATAAAAATTTACTA 1315
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SCHMITT, Manfred
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Pred. No. 0.00017;
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Sequence 592, Application US/11033545

SERIERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000790

CURRENT APPLICATION NUMBER: US/11/033,545

CURRENT APPLICATION NUMBER: US/11/033,545

CURRENT FILING DATE: 2005-09-08

NUMBER OF SEQ ID NOS: 10823

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 592

LENGTH: 18651
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Best Local Similarity 48.8%;
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ORGANISM: Human
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                                                                                           TAAGATTATAATCTATGTTATAATGATAATATATTTTAAAAATAATACTATATTAATT
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                                                               TATTAATTTAACTTAATTTAATTTAATATATATAATAT--AAATTTTAATATTTTAAT 1023:
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RESULT 5
US-11-033-545-786
; Sequence 786, Application US/11033545
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS:
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO0790
CURRENT APPLICATION NUMBER: US/11/033,545
CURRENT APPLICATION NUMBER: US/11/033,545
CURRENT FILING DATE: 2005-01-12
PRIOR APPLICATION UNMER: 60/231,401
PRIOR APPLICATION UNMER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FRASESEQ for Windows Version 4.0
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Best Local Similarity 48.8%;
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ORGANISM: Human
-11-033-545-786
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             AATTTAAAATAAATTATTGAGCATGGGAAGTT 1712
                                                              AAATTTTAATATTTTTÄTTTTÄÄTÄTTÄÄÄTTÄAÄÄTTTTÄÄTTTÄÄÄATTTAÄATTTAÄÄTTTÄ
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                                                                                                                                                                                                              TTTAATATTAATTTAATATTAAATTAAATTTTÄATTTTTÄATTTTAATATTAATTTÄÄ 10311
                                                                                                                                                                                                                                                  CTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATGAATAAATCAG 1560
                                                                                                                                                                                                                                                                                       TATTAATTIAACTTAATTTAATTTAATTTAATATTAAATT--AAATTTTAATATTTTAAT 10251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18682;
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US-10-517-441-293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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473; Conserv
GGTAAAGTAGCGGGACCCACCAATATATAATTGATAGATTTAGAAAAGTAGTTGAAAGTA 1277
                                                                                                          MARTENS, John
MODEL, Fabian
NIMMRICH, Inko
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APPLICANT: RUDAN, Tamas

APPLICANT: SCHMITT, Armin

APPLICANT: SCHMITT, Manfired

APPLICANT: LOOK, Maxime P.

APPLICANT: LOOK, Maxime P.

APPLICANT: HOEFLEK, Heinz

ITILE OF INVENTION: Method and nucleic acids for the company of th
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                                                                            1098 TTTGAAAAAACAAATAGGTACTCCCTCCGTCCCTCTGAAATGTATACATATGGATTGGAC 1157
                                                                                                                                                                                                                                                                      1038 СТТСТТАЛААСАЛАТТСААТСАСАТАЛАЛАТАТСТТАСАЛТСАЛАДАЛАСАЛССАЛТСТСТС 1097
ATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACT-GATCATCCATTAAAAC 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAGAAATTTAGTACAGGTTAAAACTTTTACAAGAATTTATATTAAACGAAAATCATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67.4; DB 7;
Pred. No. 0.00074;
0; Mismatches 581
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APPLICANT: HOEFLER, Heinz
TITIE OF INVENTION: Method and nucleic acids for
ITITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR APPLICATION NUMBER: DE 103100096.8
                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-10-517-441-567
; Sequence 567, Applic;
; GENERAL INFORMATION:
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APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
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MODEL, Fabian
NIMMRICH, Inko
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SCHMITT, Armin
SCHMITT, Manfred
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PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 567
LENGTH: 5286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                 TAATATAAAAGTAAATTTTAAATTAATTGTTATTTTTTGTTTCAGAA-ATTTAAAATAAAT 1694
                                                                                            ATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTTCATGTGTATTCAATAGTTT 1635
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Pred. No. 0.00074;
0; Mismatches 581;
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CURRENT APPLICATION NUMBER: US/10/517,441

CURRENT FILING DATE: 2004-12-11

PRIOR APPLICATION NUMBER: PCT/EP2003/010881

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-01-07

PRIOR FILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: DE 1030096.8

PRIOR APPLICATION NUMBER: DE 10245779.4

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-01

SEQ ID NO 294

LENGTH: 5286
                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                           Query Match 3.3%;
Best Local Similarity 44.7%;
Matches 450; Conservative
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US-10-517-441-294
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APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
FILE REFERENCE: 47675-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 294, Application US/10517441 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                CAGGTAAAAACAAGAGCTTGCTGCTGTGTGTTTAGTTGTTGTGAGGCTCATTTCTTTAAAA 894
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NIMMRICH, Inko
RUJAN, Tamas
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KOENIG, Thomas
MAIER, Sabine
MARTENS, John
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Pred. No. 0.00088;
0; Mismatches 535
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        Sequence 5.68, Application US/10517441
GENERAL INFORMATION:
APPLICANT: FOREMS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: KOENIG, Thomas
APPLICANT: MATERS, John
APPLICANT: MATERS, John
APPLICANT: MODEL, Fabian
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: HORFLER, Heinz
TITLE OF INVENTION: Method and nucleic
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US-10-517-441-568
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CURRENT PERLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR RILING DATE: 2003-10-01
PRIOR PILING DATE: 2003-10-01
PRIOR PILING DATE: 2003-04-17
PRIOR RILING DATE: 2003-04-17
PRIOR PILING DATE: 2003-04-17
PRIOR PILING DATE: 2003-01-07
PRIOR PILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
PRIOR PILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
PRIOR PILING DATE: 2002-10-01
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: chemically treated genomic
US-10-517-441-568
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Best Local Similarity
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AGTGTATAGAATTAAATGGGACAGAGGGAGTAATACCTTTATGATAT------AT 1417
                                                                               TTTACTATTTTGAGAAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGAA 1368
                                                                                                                                         CCTCTGAAATGTATACATATGGATTGGACACGGAGACTAAGAAAAATGTATAAAGTAATG
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Pred. No.
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US-60-655-875-1533/c
; Sequence 1533, Application US/60655875
; GENERAL INFORMATION:
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, NAME/KEY: misc feature
; LOCATION: (3964)..(3964)
; OTHER INFORMATION: n is a,
US-60-655-875-1533
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CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 1533
LENGTH: 3999
TYPE: DNA
ORGANISM: Heterodera glycines
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 201; Conserv
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TITATGATATATATATTTTGTTATTTTGATTTCATAAGATTATAAATCTATGTTATAAAT 1465
                                                                                 GAGTGGGACATCCATAAAAGGAAAGTGTATAGAATTAAATGGGACAGAGGGAGTAATACC 1405
                                                                                                                   GGGGGATTTTTATTTTAAATAATTTCTAAATTTTTATCTAATCTTCGATTTTTAGCGGATA
                                                  AAATATTAAAATGAATGAAGGAGAGATTTTCTAATTTAAGGTAATTAAATTATTTTTT 774
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Lu, Maolong
McCarter, James
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Williams, Deryck
Vaudin, Mark
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Pred. No. 0.0013;
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; ORGANISM: Homo Sapiens
US-10-517-441-24
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CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR TILING DATE: 2003-10-01
PRIOR PRILING DATE: 2003-04-17
PRIOR PFLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR PPLICATION NUMBER: DE 10300096.8
PRIOR PPLICATION NUMBER: DE 1030096.8
PRIOR PILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
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US-10-517-441-24
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Best Local Similarity
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SEQ ID NO 24
LENGTH: 5286
                                                                                                                                                                                                                                            Matches
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GENERAL INFORMATION:
APPLICANT: FOEKENS, John
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TITLE OF INVENTION: Method and nucleic acids
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
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                              TCTTTGAAAAAACAAATAGGTACTCCCTCCGTCCCTCTGAAATGTATACATATGGATTGG 1155
                                                                                                                   TTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACTTACT-GATCATCCATTAAA
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MAIER, Sabine
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ilarity 44.9%;
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Pred. No. 0.0017;
0; Mismatches 546;
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APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: ASHIKARI, TOSHIHIKO
ITILE OF INVENTION: METHODS FOR ANALYZING GENES OF IFILE REFERENCE: 030685-043
CCURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTMARE: Patentin version 3.3
SEQ ID NO 166179
LENGTH: 8391
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US-10-517-441-564
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; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-166179
                                                                                                                               APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Pabian
APPLICANT: NIMMRICH, Inko
APPLICANT: RUJAN, Tamas
                                                                                                                                                                                                                                                                    Sequence 564, Application US/10517441 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.1%;
Best Local Similarity 45.8%;
Matches 302; Conservative
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMRICH, Inko
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almuth
APPLICANT: MOBILER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
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APPLICANT:
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APPLICANT:

Lu, Maolong McCarter, James Miller, Nancy Williams, Deryck Vaudin, Mark

APPLICANT:

Boukharov, Andrey

Du, Zijing

Guo, Liang Kovalic, Da

David

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CURRENT APPLICATION NUMBER: US/10/517,441
CUBRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR PILLING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 564
LENGTH: 16579
US-60-655-875-7091/c
; Sequence 7091, Application US/60655875
; GENERAL INFORMATION:
                                                            RESULT 14
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                    АТАСТСАСТААТАТСААТААТСАСТТАТСТСААЛААССААТААТАТСТТТСТААЛАСАС 1595
                                                                                                                                                                                                                                                                                                                                                                                                        TITTAAAATAATACTATATTAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTACA 1535
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                                                                                                                      AATTAGTAAATATAATTTTTTTA 4716
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ilarity 45.5%;
Conservative
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Pred. No. 0.0027;
0; Mismatches 274;
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; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONT
; TITLE OF INVENTION: IN PLANTS AND COMPOSITI
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 7091
; ENOTH: 2421
; TYPE: DNA
; ORGANISM: Heterodera glycines
US-60-655-875-7091
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US-10-517-441-290
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APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EB2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR APPLICATION NUMBER: DE 10300096.8
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Local Similarity 49.5%;
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MAIER, Sabine
MARTENS, John
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                                                                                                                                                                              MARX, Almuth
                                                                                                                                                                                                              RUJAN, Tamas
SCHMITT, Armin
SCHMITT, Manfred
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                                                                                                                                                                                                                                                                                                                                           HARBECK, Nadia
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Pred. No. 0.0041;
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Search completed: March 15, Job time: 1980.74 secs

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PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 290
LENGTH: 16579
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
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Local Similarity 45.3%;
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                                                          ATTTAGTTTTATTTATTTTTTTTTTAGAATATATATATTTTGGAGAATGTTTTA
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Pred. No. 0.0053;
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-911-434A-1
US-09-352-608-6
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US-09-349-016-12976
US-09-949-016-15853
US-09-949-016-12387
US-09-949-016-12725
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22, Appl
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14164, A
22, Appl
15851, A
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15940, A
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Patent No. 5959176
GENERAL INFORMATION:
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US-08-911-434A-2
  Query Match
Best Local Similarity
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US-09-949-016-13248	US-09-949-016-11934	US-09-949-016-16110	US-09-949-016-156535	US-09-949-016-146404	US-09-949-016-146136	US-09-949-016-145868	US-09-949-016-37164	US-09-949-016-37150	US-09-949-016-30531	US-09-949-016-146404	US-09-949-016-146403	US-09-949-016-146136	US-09-949-016-146135	US-09-949-016-145868	US-09-949-016-145867	US-09-949-016-37164	US-09-949-016-37163
Sequence 13248, A	Sequence 11934, A	Sequence 16110, A	Sequence 156535,	Sequence 146404,	Sequence 146136,	Sequence 145868,	Sequence 37164, A	Sequence 37150, A	Sequence 30531, A	Sequence 146404,	Sequence 146403,	Sequence 146136,	Sequence 146135,	Sequence 145868,	Sequence 145867,	Sequence 37164, A	Sequence 37163, A

ALIGNMENTS

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US-08-911-434A-2
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Raymond C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 2185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)205-8000
TELEPAX: (703)205-805
INFORMATION FOR SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNABER: US/08/911,434A
FILING DATE: 12-AUG-1997
CLASSIFICATION: 800
ATTORNEY/AGENT TO THE PORTY AGENTY AGENTY AGENTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22040
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TORIKAI, Satomi
APPLICANT: OEDA, Kenji
TITLE OF INVENTION: PLANT PROMOTER AND UTILIZATION THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       MOLECULE TYPE: DN
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: nucleic acid
                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VIRGINIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                          ORGANISM: Daucus carota L. INDIVIDUAL ISOLATE: Kuroda
                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                   DNA (genomic)
11.8%;
72.8%;
                                                                                                                                                   Kuroda Gosun
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Score 241.2; DB 2
Pred. No. 5.4e-42;
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                      Length 2042;
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RESULT 2
US-08-911-434A-1
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                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.
APPLICATION NUMBER: US/08/911,434A
FILING DATE: 12-AUG-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Raymond C.
REGISTRATION NUMBER: 21,066
REFERENCE/DOCKET NUMBER: 2185-0199P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 5959176
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             TELEPHONE: (703)205-8000
TELEFAX: (703)205-8050
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART,
STREET: P.O. BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TORIKAI, Satomi
APPLICANT: OEDA, Kenji
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                              TELEPHONE:
                                                                                                                                                                                                                                                                                             COUNTRY:
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CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                          UNITED STATES OF AMERICA
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N: PLANT PROMOTER AND UTILIZATION THEREOF
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APPLICANT: ISHIGE, Fumiharu
APPLICANT: NISHIGE, Fumiharu
APPLICANT: NISHIGE, Fumiharu
APPLICANT: OEDA, Kenji
ITITLE OF INVENTION: Plant Promoter
FILE REFERENCE: 2185-0353P
CURRENT FILING DATE: 1990-07-13
EARLIER APPLICATION NUMBER: 10-200372 JAPAN
EARLIER APPLICATION NUMBER: 10-200372 JAPAN
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 20
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 246
                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Daucus carota
US-09-352-608-2
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US-09-352-608-2
                                                                                                                           Query Match
Best Local S
Matches 222
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Best Local Similarity
Matches 223; Conserv
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TYPE: nucleic acid
STRANDEDNESS; single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
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                               1865
                                                                     1805 TCTAGAATACATCITTTCAAATTTCAACAAACAACAGCTTTAACTTTTCTTTCAACGGATT 1864
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LOCATION:
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Similarity 89.5%;
22; Conservative
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AGAATCGTTTCCTAAACTTTTAAAATT.
        GGAATCCTTTTCTAAACTTTTTAAAATAAAAAAAATGCATTATTGTAATATTTATCAACA 1924
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                                                   TCTAGAATATCTTTTGAAATTTCAACAAACACAGCACTAACTTTTCTTTTAACAGATT
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                                                                                                                  Score 195.6; DB 3;
Pred. No. 1.7e-32;
0; Mismatches 24;
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Pred. No. 1e-32;
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US-09-352-608-7/c

| Sequence 7, Application US/09352608 |
| Patent No. 6218598 |
| GENERAL INFORMATION: |
| APPLICANT: ISHIGE, Fumiharu |
| APPLICANT: NISHIKAWA, Satomi |
| APPLICANT: OEDA, Kenji |
| TITLE OF INVENTION: Plant Promoter |
| PILE REFERENCE: 2185-0353P |
| CURRENT APPLICATION NUMBER: US/09/352,608 |
| CURRENT APPLICATION NUMBER: 10-200372 JAPAN |
| EARLIER APPLICATION NUMBER: 10-200372 JAPAN |
| EARLIER FILING DATE: 1998-07-15 |
| RUMBER OF SEQ ID NOS: 20 |
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US-09-352-608-6
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CURRENT APPLICATION NUMBER: US/09/352,608
CURRENT FILING DATE: 1999-07-13
EARLIER APPLICATION NUMBER: 10-200372 JAPAN
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 20
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6
SOFTWARE: PatentIn Ver.
SEQ ID NO 7
LENGTH: 140
TYPE: DNA
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APPLICANT: ISHIGE, Fundiharu
APPLICANT: NISHIKAWA, Satomi
APPLICANT: OSDA, Kenji
TITLE OF INVENTION: Plant Promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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US-09-949-016-12776
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12776
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                                                                                                                                                                                                                                                                                                                       Matches 417;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 187169
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(187169)
OTHER INFORMATION: n = A,T,C or
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TCCGTCCCTCTGAAATGTATACATATGGATTGGACACGGAGACTAAGAAAAAATGTATAAA 1182
                                                                                                                                                   ATAATAGGGATCACTTACTGATCATCCATTAAAACCTTGTTAAAACAAATTCAATGAGAT 1062
                                                                                                                                                                                                                  CTTTTACAAGAATTTATATTAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATT 1002
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                                                 Conservative
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92.6%;
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                                                                                                                                                                                                                                                                                                                                      Score 81.4; DB 4;
Pred. No. 1.4e-07;
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Sequence 15940, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307

CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 05/241,755
PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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US-09-949-016-15940
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                                                                         NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 15940
 FEATURE: misc_feature LOCATION: (1)...(191569)
                                        TYPE: DNA
ORGANISM: Human
                                                                ENGTH: 191569
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Best Local Similarity
Matches 417; Conserv
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                        ATTGAGCAGCACTAGACTGTTTGAACAATGTATGTCCGGTGTACATCTATGACCTTTCAA
                                                                            AATAATACTATATTAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGA
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Pred. No. 1.4e-07;
0; Mismatches 496;
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Sequence 15851, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FastSEQ for Windows Version 4.0
LENGTH: 205044
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; ORGANISM: Human
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(205044)
; OTHER INFORMATION: n = A,T
US-09-949-016-15851
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Best Local Similarity
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TATATATATTTAAATATAAATATATAAAAATATATTTA 201098
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                                                                AATAAATCAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAA----
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                                                                                              ----ATGGGAAGTTCATGTGTATTCAATAGTTTTAATATAAAAGTAAATTTTAAATTAA 1661
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Pred. No. 1.3e-05;
0; Mismatches 288;
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; PEATURE;
; NAME/KEY: misc_feature
; LOCATION: (1) ... (205044)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-15852
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 15852
LENGTH: 205044
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Best Local (
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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Pred. No. 1.3e-05;
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US-09-949-016-15853
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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Patent No. 6812339
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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LOCATION: (1)...(205044)
OTHER INFORMATION: n = A
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ORGANISM: Human
FEATURE:
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Similarity 48.0%;
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                          TTGTTATTTTTGTTTCAGAAATTAAAATAAATTATTGA 1700
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Pred. No. 1.3e-05;
0; Mismatches 288;
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NAME/KEY: misc_feature

LOCATION: (1)...(223471)

OTHER INFORMATION: n = A,T,C

US-09-949-016-12387
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SOFTWARE: FastSEQ for Windows V

; SEQ ID NO 12387

; LENGTH: 223471

; TYPE: DNA

; ORGANISM: Human
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-12387
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Best Local Similarity 48.0%;
Matches 278; Conservative
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12387, Application US/09949016 Patent No. 6812339
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Pred. No. 1.3e-05;
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OGANISM: Human

PEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(223471)

OTHER INFORMATION: n = A,T,C or

US-09-949-016-12724
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TITIE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FABLSEQ for Windows Version 4.0
SEQ ID NO 12724
LENGTH: 223471
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J.
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TTGTTATTTTTGTTTCAGAAATTAAAATAAATTATTGA 1700
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                                                                     ----ATGGGAAGTTCATGTGTATTCAATAGTTTTAATATAAAAGTAAATTTTAAATTAA 1661
                                                                                                      AATAAATCAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAA----
                                                                                                                                                                             TATATTAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATG 1550
                                                                                                                                                                                                                                                    TTTGATTTCATAAGATTATAAATCTATGTTATAATGATAATATAATTTTAAAAATAATAC 1490
                                                                                                                                                                                                                                                                                                                         TATÄAÄTATATÄÄÄATATÄTTTÄTATATATTTTAAATATAAATÄTÄTÄTÄÄÄÄAATATATATA
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Pred. No. 1.3e-05;
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OF DETECTION AND USES
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SOFTWARE: FASHSEQ for Windows Version
SEQ ID NO 12725
LENGTH: 223471
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(223471)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Human
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Local Similarity 48.0%;
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TATATATTTTAAATATAAATATÄTAAÄÄATATATATATTTTAAATATAAATATATAAAAA 171486
                                                                                                    AATAAATCAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAA----
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                                                                                                                                        TATATTAATTCTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATG 1550
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Pred. No. 1.3e-05;
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US-08-232-463-14/c
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3947
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DORNER, F.
APPLICANT: SCHBIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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AAAATGTATAAAGTAATGTAGAGTAAAAAGAAAGAGAAAAGAAAAGTGGGTAAAGTAGCGG 1230
                                                                                                                  ATAGGTACTCCCTCCGTCCCTCTGAAATGTATACATATGGATTGGACACGGAGACTAAGA 1170
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1800 Diagonal Road,
                                                                                                                                                                                                                                    3.4%; Score 69.4; DB 1; llarity 4.6%; Pred. No. 2.4e-05; Conservative 212; Mismatches 123;
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; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22
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CURRENT APPLICATION NUMBER: US/09/806,708B; CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 199-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
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TYPE: DNA
ORGANISM: Artificial
                                     1018 ТАСТВАТСАТССАТТАВАВССТТВТТАВАВСТВАВТЕСВАТВАВАТАВАТАТСТТАСВАТ 1077
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GATNINININININININININININSCCTCTRIMITMRWIMKGDGMTVRKKVKWRDTTCTYVDVWAD
                                                                                                                                                                                                                                                    RNTRTW---WABWKHSWCNNNNNNNNNNNNNNTWCHYTTANABBCYRANNNNAAARMARTC 775
                                                                                  NNNNMKAYYAHATINWGCWWNITDARRTINITTVMRRRWMTNTKTRWYSTTRR----HHYT
                                                                                                                          ATATTAAACGAAAATCATTTTATAACATGTCTCTCGGCTGTCATTATAATAGGGATCACT 1017
                                                                                                                                                                                                          ATGTAAACTGATCTAAAGCACATAGAAATTTAGTACAGGTTAAAAACTTTTACAAGAATTT
                                                                                                                                                                                                                                                                                            GTAAAAACAAGAGCTTGCTGCTGTGTGTTTAGTTGTTGAGCTCATTTCTTTAAAAGTA 897
                                                                                                                                                                                                                                                                                                                                       GAHSKRRTRHHTRTCRRTKYNNNNNNARTVYWYHHAARRWMNAWWTRTNNNNNNNNNNNNAC
                                                                                                                                                                                                                                                                                                                                                                                 AAAATTAGAGCTATTAATTAAGTTACTAATAAATAAGAGAGGTTAGTAAACAGAAAGCAG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGYAKSCATNNAMWYATTRWAAYAAAKWARWAGNNMRMYGAAAGNKWGCMAAMATMGBWW 951
                                                                                                                                                                    NNIMHAAVTTTHTDWCYKTWMNTWYWDMMTTMBTTTTRNMTTSTNMTNNNNNMWACTNN
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                                                                                                                                                                                                                                                                                                                                                                                                     1138 TGTATACATATGGATTGGACACGGAGACTAAGAAAATGTATAAAGTAATGTAGAGTAAA 1197
                             1558 CAGTTATCTGAAAAGCAAATAATATCTTTGTAAAACAGCGTTCGGTCAAATGGGAAGTT 1616
                                                                                       1498 ATTCTGATTAGTCGATTACCGCCTTTTATAATTTTACAATACTGAGTAATATGAATAAAT 1557
                                                                                                                                                   1438 ТСАТААGATTATAAATCTATGTTATAATGATAATATAATTTTAAAAATAATACTATATTA 1497
                                                                                                                                                                                                        1318 TTGAGAAAGTTTTGAAATGTATAGAATTGAGTGGGACATCCATAAAAGGAAAGTGTATAG
                                                                                                                                                                                                                                                                                                                                           359 MMRAWNNNNNWRBCKTTSWMWWMDHNNTHCTYGNNTWGSAYBMAAM$WWAAGASNBVT 300
                                                                                                                                                                                                                                                                                                            117 KMWRWTWKYM--WKAACNNNNBKAMYMRVAWMYSRDTTNTDWMMWTSDWBWHWYTVDYT 360
                                                                                                                                                                                                                                                                                                                                                                           477 AMKMWWAANNDAGAMDHWTYWMGNNTMWRRAWKMMMWGCRAYCCNNNNNRACVWHKH 418
                                                                                                                                                                                                                                                                                                                                                                                                                                     537 WWW.SGBVRMRWAGTWWWRRHWNNNNTDTRYYWWW.KRWARBTTTVVDSMCNAKSMWRGNNWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597 SWYWWYAUWMRCRDVTYTRNNTYCKSYAHSYWYWSNNAWMYRRYSARNWSSWARWTTRNN 538
119 CWMNAKAKVRTAMKHWWYYTDRYVSANNTGVRWMWMRWCMWWYSMNNRWYYRMGRKYTW 61
                                                                                                                          239 YBMYMGKHHWBWWRRABHRSWNWWWVKCRNKYMVSWHYHAMRYBKWABAVGCNNNWKDRM 180
                                                                                                                                                                                    299 YNWCWRWTYMGKTWTNNNNNKAWYYRTKTVAWCNNRYYYDTAVWTBKRNYKYCYAYBWY 240
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